SEARCH REQUEST FORM

Requestor's Name:		Serial Number:	
Date:	Phone:		Art Unit:
Search Topic: Please write a detailed statementerms that may have a special in please attach a copy of the sequence.	neaning. Give examples or re	levent citations, authors, keyv	ject matter to be searched. Define any words, etc., if known. For sequences, relevent claim(s).
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Date completed: 08-7 Searcher: Bever	ne4994	Search Site	Vendors
Terminal time: 27.		CM-1	STN
Elapsed time:		Type of Search	Dialog APS.
Total time: 2	.5	N.A. Sequence	Geninfo
Number of Searches:	2	A.A. Sequence Structure	SDC DARC/Questel
Number of Databases:	-	Bibliographic	Other CGN

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protein -9 protein search, using sw model August 28, 2003, 14:10:52; Search time 376 Seconds (without alignments) 30.092 Million cell updates/sec Copyright GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd

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Sequence: Title: Perfect score: US-09-845-738C-1 70 ITHRIHWESASLL 13

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 5580241 seqs, 870357830 residues

Total number of hits satisfying chosen parameters: 5580241

Minimum

Maximum 80 80 seq length: 0 length: 2000000000

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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(CGM2_6/ptodata/1/paa/US09_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 1, 1	1 70 100.0 13 23 US-09-845-738A-1 2 70 100.0 14 23 US-09-845-730-1	13 23 14 23	13	100.0	70	21
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ITHRIHWESASLL 13

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US-09-845-738A-1

ALIGNMENTS

sequence sequence

66880,

Sequence 1, Application US/09845738A
GENERAL INFORMATION:
APPLICANT: Jackowski, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR W.
TITLE OF INVENTION: OF 1562 DALTONS
FILE REFERENCE: 2132.040
CURRENT APPLICATION NUMBER: US/09/845,738A
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1
LENGTH: 13
TYPE: PAT
ORGANISM: Homo sapiens

US-09-845-738A-1

Ş Query Match Best Local Matches Similarity ITHRIHWESASLL 13 Conservative 100.0%; Score 70; DB 23; 100.0%; Pred. No. 0.00025;

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Mismatches

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Length 13;

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-846-349A-1
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GENERAL INFORMATION:
APPLICANT: Jackowski, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
TITLE OF INVENTION: OF 1690 DALTONS
FILE REFERENCE: 2132.042
CURRENT APPLICATION NUMBER: US/09/845,730
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PATENTIN Version 3.1
                                                                                                                                                                Sequence 1, Applicat GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 13; Conservative
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Best Local Similarity
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APPLICANT: Marshall, John
APPLICANT: Marshall, John
APPLICANT: Thatcher, Brad
TITLE OF INVENTION: Biopolymer Marker Indicative Of Disease State Having A Molecular
TITLE OF INVENTION: of 1449 Daltons
FILE REFERENCE: 2132.034
CURRENT APPLICATION NUMBER: US/09/846,349A
CURRENT FILING DATE: 2001-04-30
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SEQ ID NO 1
                             APPLICANT: Jackowski, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
TITLE OF INVENTION: OF 1777 DALTONS
FILE REFERENCE: 2132.043
CURRENT FAPLICATION NUMBER: US/09/845,735
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
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                 SOFTWARE: PatentIn version 3.1
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TYPE: PRT
ORGANISM: Homo sapiens
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RESULT 7
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; Sequence 1, Application US/09846345
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-735-1
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APPLICANT: Jackowski, George
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GENERAL INFORMATION:
APPLICANT: Jackowski, George
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/845,739
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
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APPLICANT: Jackowski, George
                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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Local Similarity 100.0%;
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Pred. No. 0.00029;
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Pred. No. 0.00031;
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US-09-846-344-1
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-846-345-1
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US-09-846-344-1
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APPLICANT: Jackowski, George
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CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
                                                                                          Query Match
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Best Local Similarity 100.0%;
Matches 13; Conservative 0
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Best Local
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TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
TITLE OF INVENTION: OF 2021 DALTONS
FILE REFERENCE: 2132.048
CURRENT APPLICATION NUMBER: US/09/846,344
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                    TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR TITLE OF INVENTION: OF 1865 DALTONS FILE REFERENCE: 2132.045 CURRENT APPLICATION NUMBER: US/09/846,345A CURRENT FILING DATE: 2001-04-30 NUMBER OF SEQ ID NOS: 1 NOS: 1 NUMBER OF SEQ ID NOS: 1 SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: BIOPOLYMER: MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR TITLE OF INVENTION: OF 1865 DALTONS
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TYPE: PRT
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                                                                                                                                   LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
                                                                         Local
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13; Conserv
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ITHRIHWESASLL 13
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                                                Score 70; DB 23;
Pred. No. 0.00033;
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Pred. No. 0.00033;
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RESULT 12
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                                                                                                       ; Sequence 943, Applical
; GENERAL INFORMATION:
; APPLICANT: Ladunga,
; APPLICANT: Spier, E
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                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Biopolymer Marker Indicative Of Disease State Having A Molecular TITLE OF INVENTION: Of 1998 Daltons FILE REFERENCE: 2132.013 CURRENT APPLICATION NUMBER: US/09/846,346A CURRENT FILING DATE: 2001-04-30 NUMBER OF SEQ ID NOS: 1 SOFTWARE: PatentIn version 3.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09846346A GENERAL INFORMATION:
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Best Local :
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Best Local Similarity
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                                   APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/846,346
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jackowski, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
TITLE OF INVENTION: OF 1998 DALTONS
APPLICANT: Dubman, Alex TITLE OF INVENTION: ISOI TITLE OF INVENTION: NUCL
                                                                        APPLICANT:
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APPLICANT: Marshall, John
APPLICANT: Yantha, Jason
APPLICANT: Vrees, Tammy
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                                                                                       Greenberg, Simon
                                                                    Brandenberger, Ralph
                                                                                                                          Ladunga, Steven Istvan
                                                     Wang, Yu
                                                                                                                                                               Application US/60242679
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 ISOLATED HUMAN SECRETED PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
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Pred. No. 0.00033;
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Sequence 66913, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
ITILE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66913
LENGTH: 770
TYPE: PRT
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2000-10-24
CURRENT APPLICATION
CONTRIBUTE: PRT
CORGANISM: HUMAN
US-60-242-679-943
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US-09-724-676A-66913
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Best Local S
Matches 13
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SEQ ID NO 66913
LENGTH: 770
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Best Local Similarity
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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                        ITHRIHWESASLL 13
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Pred. No. 0.012;
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Pred. No. 0.011;
; Mismatches
                                                                            Score 70; DB 21;
Pred. No. 0.012;
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Sequence 66911, Application US/09724676

GENERAL INFORMATION:
APPLICANT: Compugen LTD
ITILE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181, 4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 66911
LENGTH: 785
TYPE: PRT
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GENERAL INFORMATION:

APPLICANT: COmpugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 66911

LENGTH: 785
                                                                                                               Sequence 66914, Application US/09724676

GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 66914
LENGTH: 733
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                                                                   ; ORGANISM: Homo sapiens US-09-724-676-66914
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US-09-724-676-66914
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US-09-724-676A-66911
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Best Local :
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 13; Conservative 0
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Score 70; DB 21
Pred. No. 0.013;
Mismatches
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Pred. No. 0.012;
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Pred. No.
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US-09-724-676-66904
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US-09-724-676A-66914
; ORGANISM: Homo sapiens
US-09-724-676A-66904
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US-09-724-676-66904
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                                                                                    Sequence 66904, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 793
TYPE: PRT
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SOPTWARE: Patentin version 3.2
SEQ ID NO 66904
LENGTH: 804
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UNMERE: US/09/724,676
CURRENT FILING DATE: 2000-11-28
                                                  SEQ ID NO 66904
LENGTH: 804
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Best Local Similarity
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Similarity 100.0%;
13; Conservative 0
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Pred. No. 0.013;
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Pred. No. 0.013;
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RESULT 23
US-09-724-676-66908
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US-09-724-676-66907
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Sequence 66908, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 66907
LENGTH: 812
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CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66907
LENGTH: 812
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100.0%; Pred. No. 0.013;
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Pred. No.
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Sequence 66912, Application US/09724676
GENERAL INFORMATION:
APPLICAUT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UNMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66912
TYPE: PAT
ORGANISM: Homo sapiens
US-09-724-676-66912
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TITLE OF INVENTION: Variants of alternative spl
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66908
LENGTH: 822
TYPE: PRT
RESULT 26
US-09-724-676A-66912
; Sequence 66912, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternal
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US-09-724-676-66912
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US-09-724-676A-66908
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Best Local Similarity
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LENGTH: 822
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Local Similarity 100.0%;
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Similarity 100.0%; Pred. No. 0.013;
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Sequence 66902, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 66902
LENGTH: 841
TYPE: PRT
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US-09-724-676-66902
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US-09-724-676A-66902
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CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66912
LENGTH: 830
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CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 66902
LENGTH: 841
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
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ORGANISM: Homo sapiens
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100.0%; Pred. No. 0.013;
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RESULT

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; ORGANISM: Homo sapiens US-09-724-676-66909
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US-09-724-676A-66905
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-66905
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66909
LENGTH: 850
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 66905
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Best Local
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Best Local
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 849
TYPE: PRT
ORGANISM: Homo sapiens
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SOFTWARE: PatentIn version 3.2
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Local Similarity 100.0%;
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                              l Similarity 100.
13; Conservative
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                                             100.0%;
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                                             Score 70; DB 21;
Pred. No. 0.013;
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Pred. No. 0.013;
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                                                            Length 850;
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RESULT 34
US-09-724-676A-66903
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-66903
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US-09-724-676A-66909
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                                                 APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66903
LENGTH: 869
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66903
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 66909
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Best Local Similarity
Matches 13; Conserv
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ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
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                                      TYPE: PRT
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ORGANISM: Homo sapiens
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Pred. No.
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Pred. No. 0.013;
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 66906
LENGTH: 876
TYDE: PRT
RCANISM: Homo sapiens
US-09-724-676A-66906
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US-09-724-676A-66906
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TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66906
                        GENERAL INFORMÁTION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 1291814 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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OI OBS
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 12918.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
              SOFTWARE: PatentIn version 3.2
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TYPE: PRT
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Pred. No. 0.014;
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Pred. No. 0.014;
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Pred. No. 0.014;
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RESULT 40 US-09-724-676A-66880

Sequence 66880, Application US/09724676A GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen

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Sequence 66880, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spl
FILE REPERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66880
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US-09-724-676-66880
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US-09-724-676A-66876
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
RUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66876
LENGTH: 1190
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-09-724-676-66876
                                                                      Best Local Similarity
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                                                                                                                                          LENGTH: 1198
TYPE: PRT
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876 ITHRIHWESASLL 888
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100.0%; Pred. No.
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                                                                     Score 70; DB 21
Pred. No. 0.019;
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Pred. No.
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CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 66880

LENGTH: 1198

TYPE: PRT

ORGANISM: Homo sapiens

US-09-724-676A-66880

Query Match
Best Local Similarity 100.0%; Score 70; DB 21; Length 1198;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Seps 0;

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Db 876 ITHRIHWESASLL 888

Search completed: August 28, 2003, 14:21:19

Job time: 377 secs
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Result
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        US-10-379-747-2
US-10-408-765A-3010
US-10-408-765A-3010
US-10-613-520-1720
US-09-319-724B-19
US-09-319-724B-1
US-09-319-724B-1
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US-09-319-724B-1
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US-10-624-932-26
US-10-624-932-26
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PCT-US03-06859-2
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PCT-US03-06859-4
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                                                                                                                    Sequence 19, Appl
Sequence 7603, Ap
Sequence 5, Appli
Sequence 43, Appli
Sequence 1, Appli
Sequence 26, Appl
Sequence 11, Appl
Sequence 15, Appl
Sequence 2858, Ap
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26, Appl
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707, App
2864, Ap
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35.5 50.7 358 6 US-10-408-765A-2327 35 50.0 94 7 US-60-4485-460-97 35 50.0 214 6 US-10-603-113-15056 35 50.0 214 6 US-10-603-114-4555 35 50.0 337 6 US-10-603-114-6463 35 50.0 337 6 US-10-603-114-6463 35 50.0 1231 1 PCT-US02-29560A-205 35 50.0 1231 1 PCT-US02-29560A-205 35 50.0 1231 1 PCT-US02-29560A-205 35 50.0 1231 1 VS-60-487-610-1551 34 48.6 213 5 US-10-612-783-6253 34 48.6 210 6 US-10-612-783-6253 34 48.6 694 6 US-10-637-011-21 34 48.6 694 6 US-10-631-520-797 34 48.6 694 6 US-10-613-520-1213 34 48.6 694 6 US-10-341-134-26 34 48.6 758 6 US-10-341-134-28 34 48.6 768 6 US-10-341-134-26	45	44	43	42	41	40	39.	38	37	36	35	34	33	32	31	30	29	28
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	67, Appl		26, Appl	6891, Ap	1213, Ap	797, App	21, Appl	778, App	6253, Ap	1551, Ap	205, App	1310, Ap	•	6463, Ap	4555, Ap	15056, A	927, App	2327, Ap

ALIGNMENTS

CURRENT APPLICATION NUMBER: US/09/845,738C CURRENT FILING DATE: 2001-04-30 NUMBER OF SEQ ID NOS: 1 SOFTWARE: PatentIn version 3.1 SEQ ID NO 1 LENGTH: 13 TYPE: PRT ORGANISM: Homo sapiens US-09-845-738C-1 Query Match Best Local Similarity Watches 13; Conserve RESULT 1 US-09-845-738C-1 맑 á PCT-US03-06859-4 Sequence 4, Application PC/TUS0306859 GENERAL INFORMATION: Sequence 1, Applications APPLICANT: CuraGen Corporation, et al TITLE OF INVENTION: THERAPBUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS APPLICANT: Jackowski, George TITLE OF INVENTION: BLOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING TITLE OF INVENTION: OF 1562 DALTONS FILE REFERENCE: 2132.040 1 ITHRIHWESASLL 13 1 ITHRIHWESASLL 13 Application US/09845738C Conservative 100.0%; 0, Score 70; Pred. No. Mismatches DB 5; Length 13; Indels 0 Gaps A MOLECULAR 0,

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US-10-379-747-4
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PCT-US03-06859-2
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PCT-US03-06859-4
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CURRENT FILING DATE: 2003-03-05
PRIOR APPLICATION NUMBER: 60/365,034
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 60/366,420
PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: 60/365,477
PRIOR APPLICATION NUMBER: 60/365,477
PRIOR APPLICATION NUMBER: 60/365,477
PRIOR FILING DATE: 2002-03-19
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SEQ ID NO 4
LENGTH: 705
                                                                                                                                                                                                                            Sequence 2, Application PC/TUS0306859 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 70; DB 6; 1
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 13; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: PCT/US03/06859
CURRENT FILING DATE: 2003-03-06
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APPLICANT: Rieger, Daniel K.;
APPLICANT: Shimkets, Richard A.;
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: THERAPBUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
                                                                      PRIOR APPLICATION NUMBER: 10/379,747
PRIOR FILING DATE: 2003-03-05
PRIOR APPLICATION NUMBER: 60/365,034
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nes 13; Conserv
APPLICATION NUMBER: 60/365,477
                  APPLICATION NUMBER: 60/366,420 FILING DATE: 2002-03-21
                                                      FILING DATE:
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Gangolli, Esha A.;
Malyankar, Uriel M.;
Miller, Charles E.;
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Patturajan, Meera;
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                                                      2002-03-15
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RESULT 5
US-10-379-747-2
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; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-06859-2
                                                                                                                                US-09-897-516A-4590
                                                                                                                                                 RESULT 6
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US-10-379-747-2
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Best Local Similarity
Matches 13; Conserv
                                                                                            Sequence 4590, Application US/09897516A GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 45
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                              Matches
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Best Local (
                                                       APPLICANT: Corbin, David R. APPLICANT: Goldman, Barry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/365,034
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 60/366,420
PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: 60/365,477
PRIOR FILING DATE: 2002-03-19
PRIOR FILING DATE: 2002-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 21402-568B
CURRENT APPLICATION NUMBER: US/10/379,747
CURRENT FILING DATE: 2003-03-05
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APPLICANT: Chant, John S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Shimkets, Richard A.;
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD<sup>o</sup>
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13; Conserv
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Goldman, barr,
Hinkle, Gregory J.
Minkle, Joseph E.
Minkle, Joseph E.
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Edinger, Shlomit R.;
Gangolli, Esha A.;
Malyankar, Uriel M.;
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Rastelli, Luca;
Rieger, Daniel K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 70; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
                                                                                                                                                                                                                                                                            100.0%; ilarity 100.0%; Conservative 0
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Pred. No. 0.00078;
Pred. No. 0.00078;
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Huesing, Joseph E.
Malvar, Thomas M.
Krasomil-Osterfeld, Karina

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US-10-408-765A-3010
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Best Local Similarity 54.5
                                                                                                                                                                                                         Sequence 1720, Appli
GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3010:
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SEQ ID NO 4590
LENGTH: 475
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                              APPLICANT: Wu, Wei
APPLICANT: Maolong, Lu
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFERENCE: 38-77(52900)E
CURRENT APPLICATION NUMBER: US/10/613,520
CURRENT FILING DATE: 2003-07-02
PRIOR APPLICATION NUMBER: US 60/365,301
                                                                                                                                                                    APPLICANT: Monsanto Technology, LLC APPLICANT: Laurie, Cathy C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
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CURRENT FILING DATE: 2001-06-29
ERIOR APPLICATION NUMBER: US 60/215,161
PRIOR FILING DATE: 2000-06-30
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TYPE: PRT
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APPLICANT: Fahy, Eoin D.
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ITTLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

ITTLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
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TILE REFERENCE: 38-21(51847)B
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FILING DATE: 2002-03-15
APPLICATION NUMBER: US 10/389,566
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175 HQSHWQAKSLL 185
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Taylor, Steven W.
Glenn, Gary M.
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                                                                                                                                                                                                                          Application US/10613520
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54.5%;
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Pred. No.
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Pred. No.
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Query Match
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; OTHER INFORMATION: GenBank No.
US-09-319-724B-19
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                                                                                                                                                                                     Sequence 7603, Appli
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
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APPLICANT: LENZEN,
APPLICANT: STROSBE
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APPLICANT:
APPLICANT:
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                                                                  APPLICANT:
                                                                                                                                                     APPLICANT: Corbin, David R. APPLICANT: Goldman, Barry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/391,786 PRIOR FILING DATE: 2002-06-25
                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SUGASAWA, Toshinari
APPLICANT: MOROOKA, Shigeaki
TITLE OF INVENTION: MAMMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS
FILE REFERENCE: 53356-5001-US
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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mes 6; Conserv
                            CANT: Goldman, Barry S.
CANT: Hinkle, Gregory J.
CANT: Hissing, Joseph E.
CANT: Malvar, Thomas M.
CANT: Krasomil-Osterfeld, Karina C.
CANT: Steven C.
CANT: Spiridonov, Sergei
COF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
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                                                                                                                                                                                                         Application US/09897516A
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NUMBER: US/09/897,516A
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Pred. No.
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Pred. No.
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US-10-463-190-43
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US-09-319-724B-5
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PRIOR APPLICATION NUMBER: US 60/215,161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8415
SEQ ID NO 7603
                                                                                                                                                                                                          Sequence 43, Application US/10463190
GENERAL INFORMATION:
APPLICANT: Brunkow, Mary E.
APPLICANT: Galas, David J.
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         APPLICANT: Van Ness, Jeffrey
APPLICANT: Winkler, David G.
TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR
TITLE OF INVENTION: INCREASING BONE MINERALIZATION
FILE REFERENCE: 240083.508C2
CURRENT FILLING DATE: 2003-06-16
NUMBER OF SEQ ID NOS: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: STROSBERG, Arthur Donny
APPLICANT: SUGASAWA, Toshinari
APPLICANT: WOROOKA, Shjeaki
TITLE OF INVENTION: MAMMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS
FILE REFERENCE: 53356-5001-US
CURRENT APPLICATION NUMBER: US/09/319,724B
CURRENT FILING DATE: 203-07-24
PRIOR APPLICATION NUMBER: EP 96402719.7
PRIOR PILING DATE: 1996-12-12
PRIOR APPLICATION NUMBER: PCT/EP97/07339
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                            APPLICANT:
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TYPE: PRT
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nes 8; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                           52.9%;
Similarity 85.7%;
6; Conservation
FastSEQ for Windows Version 3.0
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Mulligan, John T.
Paeper, Bryan W.
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Pred. No. 75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 17;
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; TYPE: PRT; ORGANISM: Homo sapiens US-10-463-190-43
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US-10-616-263-26
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US-09-319-724B-1
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Best Local Similarity 50.0
Thes 4; Conservative
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LENGTH: 267
                                                                                                                                                                                                                                                                                                                                Sequence 26, Application US/10616263 GENERAL INFORMATION:
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APPLICANT: LENZEN,
APPLICANT: STROSBEI
APPLICANT: SUGASAW
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Best Local
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APPLICANT: SUGASAWA, Toshinari
APPLICANT: SUGASAWA, Toshinari
APPLICANT: WOROOKA, Shigeaki
TITLE OF INVENTION: MAMMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS
FILE REFERENCE: 53356-5001-US
CURRENT PAPPLICATION NUMBER: US/09/319,724B
CURRENT FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: EP 96402719.7
PRIOR APPLICATION NUMBER: P04402719.7
PRIOR APPLICATION NUMBER: P04402719.7
PRIOR APPLICATION NUMBER: P04402719.7
PRIOR APPLICATION NUMBER: P07/EP97/07339
PRIOR FILING DATE: 1996-12-12
PRIOR FILING DATE: 1997-12-12
                                                                                                                                                                                                                                                                 APPLICANT:
             TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM FILE REFERENCE: 00766,000103.5
CURRENT APPLICATION NUMBER: US/10/616,263
CURRENT FILING DATE: 2003-07-08
NUMBER OF SEQ ID NOS: 240
                                                                                                APPLICANT:
                                                                                                                                                APPLICANT:
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TYPE: PRT
ORGANISM: Homo sapiens
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PatentIn Ver.
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                                                                                                Fechtel, Kim
Genetics Institute,
                                                                                                                                               Agostino, Michael J.
Steininger II, Robert J.
Spaulding, Vikki
Wong, Gordon G.
                                                                                                                                                                                                               Merberg, David
Treacy, Maurice
                                                                                                                                                                                                                                                               LaVallie, Edward R.
Collins-Racie, Lisa A.
                                                                                                                                 Clark, Hilary
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85.7%;
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Pred. No.
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Pred. No. 40;
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RESULT 16
US-09-319-724B-15
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US-10-616-263-26
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LENGTH: 545
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PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
                                                                                                                                  SOFTWARE: PatentIn version 3.1 SEQ ID NO 15
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                                                                                                                                                                                      APPLICANT: STROSBERG, Arthur Donny
APPLICANT: SUGASAWA, Toshinari
APPLICANT: SUGASAWA, Toshinari
APPLICANT: MOROOKA, Shigeaki
TITLE OF INVENTION: MAMMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS
FILE REFERENCE: 53356-5001-US
CURRENT APPLICATION NUMBER: US 903-07-24
CURRENT FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: EP 96402719.7
PRIOR FILING DATE: 1996-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
RUMBER: OF SEG ID NOS: 21
CORTMADE: BEFORTICE: 1007-12-12
CORTMADE: 1007-12-12
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APPLICANT: SUGASAWA, Toshinari
APPLICANT: MOROCKA, Shigeaki
TITLE OF INVENTION: MAMMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS
FILE REFERENCE: 53356-5001-US
CURRENT APPLICATION UNMEER: US/09/319,724B
CURRENT FILING DATE: 2003-07-24
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APPLICANT: LENZEN
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                  TYPE: PRT
ORGANISM: Homo sapiens
EATURE:
                                                                                                ENGTH: 578
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Local Similarity 85.7%;
hes 6; Conservative
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Local Similarity 85.7%;
nes 6; Conservative
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Pred. No. 86;
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Best Local Similarity
Matches 6; Conserve
                                                               ; TYPE: PRT
; ORGANISM: Xenorhabdus sp
US-09-897-516A-5850
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US-10-603-108-2858
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; OTHER INFORMATION: SM binding protein US-09-319-724B-15
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US-09-897-516A-5850
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                                                                                                                 CURRENT APPLICATION NUMBER: US/09/897,516A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8415
SEQ ID NO 5850
LENGTH: 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 52.9%;
Best Local Similarity 50.0%;
Matches 6; Conservative
          Query Match
Best Local Similarity
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GENERAL INFORMATION:
Matches
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CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US 09/540,263
PRIOR FILING DATE: 2000-04-04
PRIOR APPLICATION NUMBER: US 60/125,416
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 3840
                                                                                                                                                                                                                                         APPLICANT: Spiridonov, Sergei TITLE OF INVENTION: Xenorhabdus sp. Genome FILE REFERENCE: 38-21(51847)B
                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Corbin, David R. APPLICANT: Goldman, Barry APPLICANT: Hinkle, Gregory
                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARITITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gary L. Breton
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 LTHWVLWETAGL 327
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6
                                                                                                                                                                                                                                                                                                      Goldman, Barry S.
Hinkle, Gregory J.
Huesing, Joseph E.
Malvar, Thomas M.
Krasomil-Osterfeld, Karina C.
                                                                                                                                                                                                                                                                                          Slater, Steven C
Conservative
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                  52.9%;
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85.7%;
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1; Mismatches
                  Score 37; DB 5;
Pred. No. 1e+02;
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Pred. No. 86;
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Gaps
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US-10-624-932-26
                              S
                                                                                                                                  US-10-624-932-26
                                                                                                                                                                                                                                                                              Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
                                                                 Matches
                                                                                              Query Match
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APPLICANT:
APPLICANT:
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APPLICANT:
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PRIOR FILLING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/222,840
PRIOR FILLING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,752
PRIOR FILLING DATE: 2000-08-08
PRIOR FILLING DATE: 2000-08-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/918,779
PRIOR FILING DATE: 2001-07-03
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                                                                                                                                              NAME/KEY: VARIANT
LOCATION: (1185)
OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
OTHER INFORMATION: specification
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                                                                                                                                                                                                                                                               ENGTH:
                                                               Local Similarity es 6; Conserv
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/225,470 FILING DATE: 2000-08-15
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/225,392 FILING DATE: 2000-08-15
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/225,146 FILING DATE: 2000-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/223,769 FILING DATE: 2000-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/223,770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-08-08
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428
                              3 HRIHWESASLL 13
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Rastelli, Luca
Spaderna, Steven
Shimkete, Richard
Zerhusen, Bryan
HRFHWSRCSKL 438
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Gerlach, Valerie
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MacDougall, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smithson,
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                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             William
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                                                                              52.9%;
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                                                               0,
                                                                              Score 37;
Pred. No.
                                                               Mismatches
                                              1.8e+02;
1.8e+02;
1.8e+02;
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                                                                                            Length 1210;
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                                                             Gaps
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APPLICANT:

APPLICANT:

Harlocker, Susan L.

Mitcham, Jennifer L.

APPLICANT: APPLICANT: APPLICANT:

Jiang, Yuqiu Henderson, Robert A. Kalos, Michael D.

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APPLICANT: DING, Li; YUE, Henry;
APPLICANT: LEE, Sally; SWARNAKAR, Anita;
APPLICANT: TRAM, Uyen K; XU, Yuming
TITLE OF INVENTION: PROTEIN MODIFICATION AND MAINTENANCE MOLECULES
FILE REFERENCE: PI-0361 USN
CURRENT APPLICATION UNMEBR: US/10/467,042
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: PCT/US02/02813
PRIOR FILING DATE: 2002-01-30
PRIOR FILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/266,762
PRIOR APPLICATION NUMBER: US 60/269,581
PRIOR APPLICATION NUMBER: US 60/271,198
PRIOR APPLICATION NUMBER: US 60/272,813
RESULT 21
PCT-US02-14753A-707
; Sequence 707, Application PC/TUS0214753A
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                   В
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US-10-467-042-4
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GENERAL INF
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SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                               Best Local Similarity Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/275,586 PRIOR FILING DATE: 2001-03-13 PRIOR APPLICATION NUMBER: US 60/278,505 PRIOR FILING DATE: 2001-03-23
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PRIOR FILING DATE: 2001-03-01
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NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 1719204CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1221
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                   434 HRFHWSRCSKL 444
                                                                                                                                                                                                                                                                                 3 HRIHWESASLL 13
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DUGGAN, Brendan M.; HAFALIA, April J.A.;
ARVIZU, Chandra S.; THANGAVELU, Kavitha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRIFFIN, Jennifer A.; GIETZEN, Kim
LU, Dyung Aina M.; ISON, Craig H.;
RAMKUMAR, Jayalaxmi; TANG, Y. Tom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GANDHI, Ameena R.; BAUGHN, GRIFFIN, Jennifer A.; GIET
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BURFORD, Neil; DELEGEANE, Angelo M.;
                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                Length 1221;
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Fanger, Gary R. Retter, Marc W.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2864, Application US/10374780A
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                         PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR APPLICATION NUMBER: 60/336,049
                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
CRICK APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
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                                                                                                                                                                                                           APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 CIP
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bes 5; Conserv
APPLICATION NUMBER: 60/338,692 FILING DATE: 2001-12-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Riechmann, Jose Luis
Jiang, Cai-Zhong
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Stolk, John F
                                                                                                                                                                                                                                                                               Pilgrim, Marsha L
Dubell III, Arnold T
                                                                                                                                                                                                                                                                                                                   Keddie, James
Broun, Pierre E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skeiky, Yasir A. W
Hepler, William T.
                                                                                                                                                                                                                                                                                                                                                                                                             Creelman,
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Heard,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craig H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                John
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                                                                                                                                                                                                                                                                                                                                                    T. Lynne
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                                                                                                                                                                                                                                                                                                                                                                                                           Robert A
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                         Oliver
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RESULT 24
US-10-293-244-1738
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US-10-603-114-4493
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 2864
LENGTH: 345
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GENERAL INFORMATION:
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Best Local Similarity
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LENGTH: 346
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GENERAL INFORMATION:
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Matches 6; Conserv
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PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,067
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,068
PRIOR APPLICATION NUMBER: 10/225,068
PRIOR FILING DATE: 2002-08-09
              CURRENT APPLICATION NUMBER: US/10/293,244
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: Not Yet Assigned
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 09/728,422
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-10-20
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CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/543,681
PRIOR FILING DATE: 2000-04-05
                                                                                                                                                                      APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y. Tom et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILITILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2002-06-14
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ORGANISM: Arabidopsis thaliana
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09/663,561
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Pred. No.
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Pred. No.
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CURRENT APPLICATION UMBER: US/10/612,783
CURRENT FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 7098
SEQ ID NO 5264
LENGTH: 356
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
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US-10-293-244-3486
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Best Local Similarity
Thes 6; Conserve
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US-10-293-244-1738
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PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalio, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53373)A
GUIDDREW ADVICANT STAN AUGUST 100.
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SOFTWARE: Custom
SEQ ID NO 1738
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Best Local (
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APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y. Tom et al
APPLICANT: Tang, Y. Tom et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-029
CURRENT APPLICATION NUMBER: US/10/293,244
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: Not Yet Assigned
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 09/728,422
PRIOR APPLICATION NUMBER: 09/728,422
PRIOR FILING DATE: 2000-11-30
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APPLICATION NUMBER: 09/654,936
FILING DATE: 2000-09-01
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5; Conserve
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Pred. No.
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Pred. No.
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76;
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CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: Not Yet Assigned
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 09/728,422
PRIOR FILING DATE: 2000-11-30
PRIOR PPLICATION NUMBER: 09/693,325
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/663,561
PRIOR FILING DATE: 2000-09-16
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/620,325
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US-10-293-244-1518
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SOFTWARE: CUBLC
SEQ ID NO 3486
'FNGTH: 272
                                                                              Query Match 50.7%;
Best Local Similarity 47.1%;
Matches 8; Conservative
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APPLICANT: Tang, Y. Tom et al
TITLE OF INVENTION: Novel Nucleic Acids and
FILE REFERENCE: 21272-029
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PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/620,325
PRIOR APPLICATION NUMBER: 09/620,325
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PRIOR FILING DATE: 2000-02-03
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PRIOR FILING DATE: 2000-04-27
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PRIOR FILING DATE: 2000-06-20
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TYPE: PRT
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les 8; Conserv
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2 THR-----IHWESASLL
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Pred. No. 72;
1; Mismatches
                                                                                                          Score 35.5;
Pred. No. 9:
                                                                                   Mismatches
                                                                                                          95;
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                                                                                                                                   Length 358;
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RESULT 28

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SHRPVGMDIHWEKVSKL 271

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RESULT 30
US-10-603-113-15056
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US-60-485-450-927
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US-10-408-765A-2327
Sequence 15056, Application US/10603113
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2327
LENGTH: 358
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 47859
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 927
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Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2003-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CARGILL, Michele
APPLICANT: CHANG, Sheng-Yung
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: WIRUS-INFECTED SUBJECTS, METHODS OF I
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CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: VIRTUITLE OF INVENTION: THE FILE REFERENCE: CL001470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
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                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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Pred. No. 30;
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Pred. No. 9
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METHODS OF DETECTION AND USES
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US-10-603-114-4555
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US-10-603-114-6463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Candida albicans US-10-603-113-15056
                               TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILITITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION UNMEER: US/10/603,114

CURRENT FILING DATE: 2003-06-24

PRIOR APPLICATION NUMBER: US/09/543,681

PRIOR APPLICATION NUMBER: US/09/543,681

PRIOR FILING DATE: 2000-04-05

PRIOR FILING DATE: 2000-04-05

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 6463

LENGTH: 337

TYPE: PRT
                                                                                                                                                                                                                                                                                                     Sequence 6463, Application US/10603114 GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: GARY BRE
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SEQ ID NO 4555
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Best Local
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FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/10/603,114
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/543,681
PRIOR APPLICATION NUMBER: US/09/543,681
PRIOR PILING DATE: 2000-04-05
PRIOR PILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
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PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 28206
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CURRENT FILING DATE: 2003-06-24
                                                                                                                                                                                                                                                                                     APPLICANT: GARY BRETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 107196.132
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TYPE: PRT
               ORGANISM: Proteus mirabilis
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5; Conserv
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Pred. No.
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Pred. No.
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189
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Query Match

50.0%;

Score 35;

DB 6;

Length 337;

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RESULT 35
PCT-US02-29560A-205
Sequence 205, Application PC/TUS0229560A
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                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Marches 5; Conserve
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US-60-487-610-1550
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APPLICANT: HUANG, Hongiin
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1550
LENGTH: 566
TYPES. DETECTION TO THE PROPERTY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1310
LENGTH: 1386
TYPE: PRT
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APPLICANT:
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TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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                                                                                                                                                                84 LLHLIHWE 91
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Taylor, Steven W.
Glenn, Gary M.
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Pred. No. 1.8e+02
0; Mismatches '
                                                                                                                                                                                                                                                                                                                    Score 35; DB 6;
Pred. No. 3.5e+02;
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RESULT 37
US-10-612-783-6253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CARGILL, Michele
APPLICANT: HUANG, Hongjin
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1551
LENGTH: 1211
TYPE: DRT
USES CLOSES
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 205
LENGTH: 1211
                                                                                                                                                    Sequence 6253, Application US/10612783 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 55.6%; Matches 5; Conservative
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-002710PC
CURRENT APPLICATION NUMBER: PCT/US02/29560A
CURRENT FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: US 60/323,469
PRIOR FILING DATE: 2001-09-17
                                                           APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovallc, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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APPLICANT: Aziz, Natasha
APPLICANT: Gish, Kurt C.
APPLICANT: Hevezi, Peter
                  TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
TITLE OF INVENTION: Plants FILE REFERENCE: 38-21(53373)A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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Mack, David H.
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Pred. No. 3.9e+02;
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Pred. No. 3.9e+02;
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US-10-637-011-21
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CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 3264
SOFTWARE: PatentIn version 3.2
SEQ ID NO 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/612,783
CURRENT FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 7098
SEQ ID NO 6253
LENGTH: 210
TYPE: PRT
                                                                                                                                                    Sequence 21, Application US/10637011 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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Best Local Similarity 62.5%;
                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Institute for Genomic Research
APPLICANT: Chiron Corporation
TITLE OF INVENTION: Neisseria Meningitidis Antigens and Compositions
                                                    APPLICANT:
                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: CHIR-0334
                                                                  APPLICANT:
                                                                                                                                      APPLICANT: JESTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: (23)...(23) OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
LOCATION: (1)..(210)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (35)...(35)
OTHER INFORMATION: Xaa can be any naturally occurring amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Clone ID: PAT_MRT4577_78571C.1.pep
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TYPE: PRT
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ARNAULD, Claire
TRUONG, Catherine
MAHE, Dominique
CARIOLET, Roland
                                                                              ALBINA, Emanuel
Le CANN, Pierre
BLANCHARD, Phillipe
                                                                    HUTET, Evelyne
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Pred. No. 1e+02;
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Pred. No. 98;
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                                                                                                                                                         ; TYPE: PRT ; ORGANISM: Oryza sativa US-10-613-520-797
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US-10-613-520-797
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SEQ ID NO 21
LENGTH: 566
TYPE: PRT
                                                                          Query Match
Best Local Similarity
Matches 5; Conserv
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APPLICANT: Monsanto Technology, LLC
APPLICANT: Laurie, Cathy C
APPLICANT: Wu, Wei
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Best Local Similarity
Matches 4; Conserv
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SEQ ID NO 797
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                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/613,520
CURRENT FILING DATE: 2003-07-02
CURRENT PRICATION NUMBER: US 60/365,301
PRIOR APPLICATION NUMBER: US 60/365,301
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 10/389,566
PRIOR FILING DATE: 2003-03-14
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CURRENT FILING DATE: 2003-08-08
PRIOR APPLICATION NUMBER: US/09/514,245B
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: FR 97/15396
PRIOR FILING DATE: 1997-12-05
                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 2578
                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR FILING DATE: 2002-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Maolong, Lu
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFERENCE: 38-77(52900)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 170
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                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/391,786
                                                                                                                                                                                                                   ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             510 HOLHWKEKEL 519
    44
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RLHWERRGLV
                                    RIHWESASLL 13
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                                                                              Conservative
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                                                                                                Score 34; Pred. No. 3
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Pred. No. 2.7e+02;
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                                                                                                                Length 694;
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Search completed: August 28, 2003, 14:21:50 Job time: 24 secs

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Maximum DB seq length: 200000000
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Perfect score:
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A Geneseq 19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
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3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	100.0 1540 22 ABG25976 100.0 1592 18 AAW34623		100.0 14 24 ABP58087 100.0 15 24 ABG75803	y h Length DB ID
Human C3 protein m Human C3 protein m	human diagn	Disease specific b Congestive heart f	Complement C3f fra	Description

Biopolymer marker useful for evidencing, categorizing or regulating least one disease state, e.g. congestive heart failure, myocardial

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5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
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ABP29330	ABB69833	AAG15895	ABP10890	ABB54019	ABB58617	ABG72971	ABU08967	AAW34631	AAW34626	AAW34618	AAW34617	AAW34616	AAW34615	AAW34614	AAW34613	AAW34612	AAW34611	AAW34610	AAW34609	AAW34608	AAW34607	AAW34606	AAW40990	AAW40989	AAW40988	AAW34630	AAW34628	AAW34627	AAW34621	AAW34620	AAW34619	AAR94030	AAR94029	AAR94028	AAW34625
Streptococcus poly	Drosophila melanog			Lactococcus lactis	phila m	Human complement C	Human complement C	G		ជ	C3 protein		protein	C	C	C	Human C3 protein m	C	C3 protein	C	n C3 proteir	type human C	C	C3 protein	C	C		•	Human modified C3	Human C3 precursor	Human C3 protein m				

ALIGNMENTS

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RESULT 1
ABP58087
ID ABP5
XX ABP5
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XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                 WPI; 2003-111907/10.
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                                                                                                                                                                                                                                                                                                                                                                                                               30-APR-2001; 2001US-0845730.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complement C3f fragment, specific disease marker.
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                                                                                                                                                                                                                                                                                                                        (SYNX-) SYN.X PHARMA INC.
                                                                                                                                                                                                                             Thatcher B,
                                                                                                                                                                                                                             Vrees T,
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infarction or

intracerebral hemorrhage

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preparatory steps in conjunction with mass spectroscopy and time-of-flight detection procedures to maximise the diversity of biopolymers which are verifiable within a particular sample. The cohort of biopolymers verified within such a sample is then viewed with reference to their ability to evidence at least one particular disease state, thereby enabling a diagnostician to gain the ability to characterise either the presence or absence of a disease state relative to recognition of the presence and/or absence of the biopolymer. Diagnostic assay kits including the present biopolymer marker are claimed, and a process for regulating a disease state by controlling the presence or absence of the biopolymer marker is
                                                                                                                                                                                                                                                                           31-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                        Biopolymer; disease state; congestive heart failure; asymptomatic; diabetes; kidney failure; heart failure; Syndrome X; heart attack; stroke; C3f; complement system.
                                                                                                                                                                                                                                                                                                                                                                                                              Congestive heart failure C3f fragment marker bioploymer.
                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG75803 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       about 1690 Da. The marker is indicative of an individual suffering from myocardial infarction, intracerebral haemorrhage or congestive heart failure. The invention involves the use of a combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
            Claim 1;
                                      disease state
                                                                                                        Jackowski G,
                                                                                                                                                 (JACK/)
(THAT/)
(MARS/)
(YANT/)
                                                                                                                                                                                                                    30-APR-2001; 2001US-0845739
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                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in indicating at least one particular disease state. The mar
                                   novel biopolymer marker useful in indicating at least one particular isease state particularly congestive heart failure -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                               2003-246643/25.
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                                                                                                                                                 THATCHER B.
MARSHALL J.
YANTHA J.
                                                                                                                                                                                          JACKOWSKI G.
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ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence is that of a biopolymer marker that is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
A
          7; 10pp; English
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                                                                                                          Thatcher
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                                                                                                        'n
                                                                                                        Marshall J,
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Pred. No. 3.4e-05;
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                                                                                                          Yantha
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                                                   least one particular disease state. (I) is useful for indicating a disease state, in particular type II diabetes. The marker sequences are useful as antigens in immunoassays for the detection of those individual suffering from the disease known to be evidenced by the marker sequence. (I) provides an efficient diagnostic tool for rapidly and accurately diagnosing disease states such as type II diabetes. This is the amino acid sequence of a biopolymer marker.
                                                                                                                                                                                                                                                                                                                                                                                                                   Biopolymer marker useful in indicating disease state, in particular type II diabetes and as antigens in immunoassays for detecting individuals suffering from disease known to be evidenced by marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disease specific biopolymer marker #1.
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                                                                                                                                                                                                                                                                   The invention describes a biopolymer marker (I) useful in indicating
                                                                                                                                                                                                                                                                                                                             Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-328370/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jackowski G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (JACK/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biopolymer marker; type II diabetes; immunoassay.
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MARSHALL J.
YANTHA J.
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3.7e-05;
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Sequence

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Best Local
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Biopolymer marker; type II diabetes; immunoassay.
                    Disease specific biopolymer marker
                                                                ABU08618;
                                                                                  ABU08618 standard; peptide;
                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                      Claim 1; Fig
                                                                                                                                                                                                                                                                                                                                         Use of biopolymer marker for evidencing, categorizing or regulating least one disease state, e.g. congestive heart failure \,
                                           23-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                               Jackowski G,
                                                                                                                                                                                                                                                                                                                                                                                                                                         30-APR-2001; 2001US-0845736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biopolymer; marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Congestive heart failure indicative biopolymer marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                    (SYNX-) SYN.X PHARMA INC
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                                                                                                                                                                                                                          17 AA;
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|llarity 100.0%;
|Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                               Thatcher
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                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                      English.
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bred. No. 4.2e-05;
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RESULT 6
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Best Local
                   31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a biopolymer marker (I) useful in indicating at least one particular disease state. (I) is useful for indicating a disease state, in particular type II diabetes. The marker sequences are useful as antigens in immunoassays for the detection of those individual suffering from the disease known to be evidenced by the marker sequence. (I) provides an efficient diagnostic tool for rapidly and accurately diagnosing disease states such as type II diabetes. This is the
                                                    30-MAR-2001; 2001WO-US08631
                                                                           11-OCT-2001
                                                                                                                                                                           Novel human diagnostic protein #25967.
                                                                                                                                                                                                    18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biopolymer marker useful in indicating disease state, in particular type II diabetes and as antigens in immunoassays for detecting individuals suffering from disease known to be evidenced by marker sequence
                                                                                                WO200175067-A2
                                                                                                                                                                                                                                              ABG25976 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence
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MARSHALL
YANTHA J.
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Pred. No.
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(HYSE-) HYSEQ INC.

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RESULT 7
AAW34623
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations constituted because of the traits to assess biodiversity and to produce other types of data and products dependent on DNA and canno acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO control of the control of t
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Matches
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                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                       Human; C3 protein; convertase; complement pathway protein; infection; down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                     Human C3 protein mutant FT-1.
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                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                   complement-mediated response; MHC-mismatched lymphocyte; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW34623 standard; Protein; 1592 AA
                        WO9732981-A1
                                                                                                                                                                                      Misc-difference
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13; Conserv
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                                                                    /note= "A1593Stop mutation'
                                                                                                               note= "E1592N mutation"
                                                                                                                                                             note= "R1591T mutation"
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Pred. No. 0.0064;
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CC forms a down-regulation resistant C3 convertase. (A), their variants, contemporary regulation resistant C3 convertase. (A), their variants, cC fragments and conjugates are used to deplete levels of complement CC parthway proteins (by superactivation until one or more components are CC exhausted), specifically to prevent rejection of foreign material CC diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous CC complement protein conversion and deposition at a specific site (e.g. a C virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application is eliminating CC contemplated is ex vivo treatment, especially by passing blood through a CC contemplated is ex vivo treatment, especially by passing blood through a CC contemplated is ex vivo treatment, especially by passing blood through a CC contemplated is ex vivo treatment, especially by passing blood through a CC contemplated is ex vivo treatment, especially by passing blood through a CC contemplated is ex vivo treatment, especially by passing blood through a CC contemplated is ex vivo treatment of the alternational anaphylactic peptides CC and other inflammatory mediators) or killing of leukaemia cells or CC minibited by factor I, it can bind repeatedly to factor B (which is then CC consumption of factor B.
Query Match
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07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
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                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a mutated human C3 protein of the invention (see AAW34606 for wild type protein). This protein is a protein of the contract of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 17; Page -; 123pp; English.
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96GB-0011896.
96GB-0014293.
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ITHRIHWESASLL 1319
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                                            100.0%;
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                                  Score 70; DB Lo;
Pred. No. 0.0066;
Pred. No. 0.0066;
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AAW34624
standard; Protein; 1635
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Human 09-APR-1998

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protein mutant FT-2.

(first entry)

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HO down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour; Homo complement-mediated disease; autoimmune disease; leukaemia cell; complement-mediated response; MHC-mismatched lymphocyte; mutein. Human; C3 protein; convertage; complement pathway protein; sapiens

Location/Qualifiers

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RESULT
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                    (particularly a xenograft) but also to prevent complement-mediated diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous complement protein conversion and deposition at a specific site (e.g. a virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application is eliminating any cancer cells left after surgical removal of a tumour). Also contemplated is ex vivo treatment, especially by passing blood through a matrix containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or MHC-mismatched lymphocytes in extracted bone marrow. Since (A) is not inhibited by factor I, it can bind repeatedly to factor B (which is then inactivated), causing inactivation of the alternative pathway by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-NOV-1996;
07-MAR-1996;
07-JUN-1996;
Human; C3 protein; convertase; complement pathway protein; infection; down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a mutated human C3 protein of the invention (see AAW34606 for wild type protein). This protein is a protein of the invention, and is a modified native complement pathway protein (A) that forms a down-regulation resistant C3 convertase. (A), their variants, fragments and conjugates are used to deplete levels of components pathway proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign material
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                                                                    Human C3 protein
                                                                                                       09-APR-1998
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13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                           1635 AA;
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                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96GB-0024028.
96GB-0004865.
96GB-0011896.
96GB-0014293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-GB00603
                                                                      mutant FR-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "wild type E mutated to stop codon"
                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                       Score 70; DB 18;
Pred. No. 0.0068;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                         <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                        Length 1635;
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                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                       0
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SAXXXX

standard;

Protein; 1661

B

AAW34625 sta AAW34625; 09-APR-1998

(first entry)

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                                         S
                                                                                                                                                                                         This sequence represents a mutated human C3 protein of the invention CC (see AAW34606 for wild type protein). This protein is a protein of the C1 invention, and is a modified mative complement pathway protein (A) that CC forms a down-regulation resistant C3 convertase. (A) their variants, CC fragments and conjugates are used to deplete levels of complement CC pathway proteins (by superactivation until one or more components are CC exhausted), specifically to prevent rejection of foreign material CC (particularly a xenograft) but also to prevent complement-mediated CC diseases resulting from (surgical) injury or antibody-antigen interaction CC in autoimmune disease, also to localise and/or amplify endogenous complement protein conversion and deposition at a specific site (e.g. a CC virus, infected cell or tumour, to increase sensitivity to CC complement-mediated responses, a particular application is eliminating CC complement-mediated responses, a particular application is eliminating CC contemplated is ex vivo treatment, especially by passing blood through a matrix containing (A) (this may remove additional anaphylactic peptides cand other inflammatory mediators) or killing of leukaemia cells or care containing (A) (this may remove additional anaphylactic peptides cand other inflammatory mediators) or killing of leukaemia cells or (A) is not contained to the contained of the contained cells or care can be contained to the contained to the contained cells or care can be contained to the contained to the contained cells or care can be contained to the contained t
                                                                                           Matches
                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-NOV-1996;
07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft
                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                         MHC-mismatched lymphocytes in extracted bone marrow. Since (A) is no inhibited by factor I, it can bind repeatedly to factor B (which is inactivated), causing inactivation of the alternative pathway by
                                                                                                                                                                                                                                   inactivated), causing consumption of factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 17; Page -; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-457534/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Farries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9732981-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement-mediated response; MHC-mismatched lymphocyte; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rejection, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IMUT-) IMUTRAN LTD.
                                                                                                                 Local
  1307
                                                                                      ch 100.0%;
1 Similarity 100.0%;
13; Conservative 0
                                         \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TC,
                                         ITHRIHWESASLL 13
ITHRIHWESASLL 1319
                                                                                                                                                                                      1657 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harrison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96GB-0024028.
96GB-0004865.
96GB-0011896.
96GB-0014293.
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1638..1645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "wild type residues QDEENQKQ mutated
                                                                                                                                                                                                                                        ω.
                                                                                           0
                                                                                                               Score 70;
Pred. No.
                                                                                        red. No. 0.0069;
Mismatches 0;
                                                                                                                                       DB 18;
                                                                                                                                     Length 1657;
                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ę
                                                                                                                                                                                                                                                                                                        (A) is not
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                                                                                           Gaps
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C

protein mutant

FT-3

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RESULT 11
AAR94028
ID AAR94
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                                                                                                                                                                                                                                                       This sequence represents a mutated human C3 protein of the invention CC (see AAW34606 for wild type protein). This protein is a protein of the cinvention, and is a modified native complement pathway protein (A) that CC forms a down-regulation resistant C3 convertase. (A), their variants, CC fragments and conjugates are used to deplete levels of complement cC pathway proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign material CC (particularly a xenograft) but also to prevent complement-mediated CC (particularly a xenograft) but also to prevent complement-mediated CC (particularly a xenograft) but also to prevent complement-mediated CC (complement protein conversion and deposition at a specific site (e.g. a Crimal of the conversion and deposition at a specific site (e.g. a CC virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application; a climinating CC contemplated is ex vivo treatment, especially by passing blood through a CC contemplated is ex vivo treatment, especially by passing blood through a CC matrix containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or CC MHC-mismatched lymphoytes in extracted bone marrow. Since (A) is not cinabilited by factor I, it can bind repeatedly to factor B (which is then can consumption of factor B.
                                                                                                                                                          Query Match
Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-NOV-1996;
07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
   AAR94028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-457534/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Farries TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; C3 protein; convertase; complement pathway protein; infection; down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour; complement-mediated response; MHC-mismatched lymphocyte; mutein.
                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 17; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rejection, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9732981-A1
                                                                                         1307
                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMUTRAN LTD.
                                                                                                                                                                           Similarity
 standard;
                                                                                                                        ITHRIHWESASLL 13
                                                                                       ITHRIHWESASLL 1319
                                                                                                                                                                                                                              1661 AA;
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harrison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96GB-0024028.
96GB-0004865.
96GB-0011896.
96GB-0014293.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1607..1614
/note= "wild type re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -; 123pp;
Protein; 1663 AA
                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "wild type residues LSSDFWGE mutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                          0
                                                                                                                                                                           Score 70; DB 18;
Pred. No. 0.0069;
                                                                                                                                                          Mismatches
                                                                                                                                                          0,
                                                                                                                                                                                         Length 1661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ť
                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEALQI'
                                                                                                                                                          Gaps
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RESULT 12
AAR94029
ID AAR94
XX
AC AAR94
XX
DT 21-MA
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                                                                                                                        Ś
                                                                                                                                                                                               Query Match
Best Local S
Matches 13
                                                                                                                                                                                                                                                     Human C3 protein (AAR94028) was produced by expression of a cDNA sequence (AAT17738) isolated from a human liver cDNA library. C3 is a complement pathway protein that is complement to cleavage by Factor I and is also susceptible to the inhibitory action of Factor H. Mutants of C3 (AAR94029 and AAR94030) have been produced by site-directed mutagenesis. These mutants can be
                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                   used to super-active the complement system, or to induce localised super-activation at a specific target to increase the target's sensitivity to complement-mediated destruction
                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                       Mutant complement pathway protein forming stable C3 convertase for generalised complement depletion or localised complement
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-171613/17.
N-PSDB; AAT17738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-1995;
08-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAY-1996
                        AAR94029;
                                             AAR94029 standard; Protein; 1663 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                            Farries TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C3 protein; convertase; Factor I; Factor H; complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human C3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR94028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IMUT-) IMUTRAN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                  Local Similarity
nes 13; Conserv
                                                                                                      1307
                                                                                                                           ITHRIHWESASLL 13
                                                                                                                                                                                               1663 AA;
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Harrison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95GB-0009102.
94GB-0018147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95WO-GB02121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             672..1663
/note= "C3 alpha chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      668..671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Sig_peptide
23..667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "amino acids 668-671 are removed when the precursor is cleaved into the alpha and beta chains"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "C3 beta chain"
                                                                                                                                                   0
                                                                                                                                                   Score 70; DB 17;
Pred. No. 0.0069;
Mismatches 0
                                                                                                                                                                          17;
                                                                                                                                                     0
                                                                                                                                                                         Length 1663;
                                                                                                                                                   0,
                                                                                                                                                   Gaps
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21-MAY-1996

(first entry)

0

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RESULT 13
AAR94030
ID AAR94
XX
AC AAR94
XX
DT 21-MA
XX
DE Human
                                                                                                                           밁
                                                                                                                                            S
                                                                                                                                                                                                                     Query Match
Best Local S
Matches 13
                                                                                                                                                                                                                                                                      A modified human C3 protein (AAR94029) differs from the wild-type (AAR94028) by substitution of Arg-1303 by glutamic acid, glycine or glutamine. It is obtained by site-directed mutagenesis of C3-encoding cDNA (AAT17738). The modification results in improved resistance to cleavage by Factor I in comparison to wild-type C3. This allows the modified C3 to be used therapeutically to
                                                                                                                                                                                                                                                                                                                                                                             Mutant complement pathway protein forming stable C3 convertase for generalised complement depletion or localised complement activation
Human modified C3 (D752G, E753S, D754G).
                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                 super-active the complement system or the increase a target's (e.g. tumour, pathogen or virus-infected cell) sensitivity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-MAY-1995;
08-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                       21-MAY-1996
                                              AAR94030;
                                                                   AAR94030 standard; Protein; 1663
                                                                                                                                                                                                                                         complement-mediated
                                                                                                                                                                                                                                                                                                                                                      Claim 8; Fig 1; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Farries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IMUT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAR-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9607738-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C3 protein;
tumour; info
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human modified
                                                                                                                           1307
                                                                                                                                                                                                                                                                                                                                                                                                                          1996-171613/17
                                                                                                                                                                      l Similarity
13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMUTRAN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection; therapy
                                                                                                                         ITHRIHWESASLL 1319
                                                                                                                                               ITHRIHWESASLL 13
                                                                                                                                                                                                                   1663 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      convertase; Factor I; Factor H; complement;
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                Harrison RA;
                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95GB-0009102.
94GB-0018147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C3 (R1303X).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95WO-GB02121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          672..1663
/note= "C3 alpha chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              668..671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Sig_peptide
23..667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Glu, Gly, Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "C3 beta chain"
                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                         destruction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "amino acids 668-671 are removed when the precursor is cleaved into the alpha and beta chains"
                                                                                                                                                                    Score 70; DB 17;
Pred. No. 0.0069;
; Mismatches 0
                                                                   ₿
                                                                                                                                                                                           Length 1663;
                                                                                                                                                                        Indels
                                                                                                                                                                      0
                                                                                                                                                                    Gaps
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RESULT 14
AAW34619
ID AAW34
XX AAW34
AC AAW34
XX 09-AE
DT 09-AE
CXX
DE Human
XX
KW Human
KW down-
KW compl
                                                                                                                                                                                    뭉
                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                     (AAR94028) by substitution of Asp-Glu-Asp at positions 752-754 igly-Ser-Gly. It is obtained by site-directed mutagenesis of C3-encoding cDNA (AAR17738). The modification reduces the interaction of C3b/C3i with Factor H in comparison to wild-type C3. This allows the modified C3 to be used therapeutically to super-active the complement system or the increase a target's (e.g. tumour, pathogen or virus-infected cell) sensitivity to complement-mediated destruction.
Human; C3 protein; convertase; complement pathway protein; infection; down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour;
                                                                                                                                                                                                                                                                                                                                                                                          A modified human C3 protein (AAR94030) differs from the wild-type
                                                  Human C3
                                                                          09-APR-1998
                                                                                                                        AAW34619 standard;
                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Fig 1; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mutant complement pathway protein forming stable C3 convertase for generalised complement depletion or localised complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                       activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-171613/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Farries TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAY-1995;
08-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAR-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C3 protein;
infection; t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMUT-) IMUTRAN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                  1307
                                                                                                                                                                                                           μ
                                                                                                                                                                                                                                  l Similarity
13; Conserv
                                                  protein
                                                                                                                                                                                                          ITHRIHWESASLL 13
                                                                                                                                                                                  ITHRIHWESASLL 1319
                                                                                                                                                                                                                                                                                 1663 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           convertase; Factor I; Factor H; complement; tumour; therapy.
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harrison
                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        precursor is obeta chains 672..1663
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94GB-0018147.
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                                                  mutant DV-9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Sig_peptide
                                                                                                                      Protein; 1663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..671
                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "C3 alpha chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "amino acids 668-671 are removed when the
                                                                                                                                                                                                                                  <u>,,</u>
                                                                                                                                                                                                                                            Score 70; DB 17;
Pred. No. 0.0069;
                                                                                                                                                                                                                                   Mismatches
                                                                                                                        Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is cleaved into the alpha and
                                                                                                                                                                                                                                                         DB 17;
                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                         Length 1663;
                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                 Gaps
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complement-mediated response; MHC-mismatched lymphocyte; mutein

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(c) (see AN34606 for wild type protein). This protein is a protein of the convention, and is a modified native complement pathway protein (A) that CG forms a down-regulation resistant C3 convertase. (A), their variants, CC fragments and conjugates are used to deplete levels of complement CC exhausted), specifically to prevent conjugates of complement CC exhausted), specifically to prevent rejection of foreign material CC (particularly a xenograft) but also to prevent complement-mediated CC diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous CC complement protein conversion and deposition at a specific site (e.g. a CC virus, infected cell or tumour, to increase sensitivity to complement cells left after surgical removal of a tumour). Also CC contemplated is ex vivo treatment, especially by passing blood through a CC contemplated is ex vivo treatment, especially by passing blood through a CC contemplated by factor mediators) or killing of leukaemia cells or CC contemplated by factor I, it can bind repeatedly to factor B (which is then CC inactivated), causing inactivation of the alternative pathway by consumption of factor B.
                                                                                                                          Query Match
Best Local
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07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complemen pathway by super-activation, especially for preventing graft
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
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1307
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                                                                                                                             Similarity
ITHRIHWESASLL 1319
                                                 ITHRIHWESASLL 13
                                                                                                                                                                                                         1663 AA;
                                                                                                  Conservative
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96GB-0004865.
96GB-0011896.
96GB-0014293.
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1219
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                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutated human C3 protein of the invention
                                                                                                    0
                                                                                                                  Score 70; DB 18;
Pred. No. 0.0069;
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RESULT 15 AAW34620

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CC fragments and conjugates are used to deplete levels of complement CC pathway proteins (by superactivation until one or more components are CC exhausted), specifically to prevent rejection of foreign material CC (particularly a xenograft) but also to prevent complement-mediated CC diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous CC complement protein conversion and deposition at a specific site (e.g. a CC virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application is eliminating CC complement-mediated responses; a particular application is eliminating CC any cancer cells left after surgical removal of a tumour). Also CC contemplated is ex vivo treatment, especially by passing blood through a matrix containing (A) (this may remove additional anaphylactic peptides CC and other inflammatory mediators) or killing of leukaemia cells or CC matrismatched lymphocytes in extracted bone marrow. Since (A) is not containing the factor I, it can bind repeatedly to factor B (which is then contactivated), causing inactivation of the alternative pathway by
Query Match
Best Local Similarity
Matches 13; Conserv
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07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathway by super-activation, especially for preventing rejection, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a mutated human C3 protein of the invention (see AAW34606 for wild type protein). This protein is a protein of the invention, and is a modified native complement pathway protein (A) that forms a down-regulation resistant C3 convertase. (A), their variants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-457534/42
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                                                                                                            consumption of factor B.
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96GB-0004865.
96GB-0011896.
96GB-0014293.
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               100.0%;
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Score 70; DB 18;
Pred. No. 0.0069;
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RESULT 16
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AAW34621
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pathway proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign material (particularly a xenograft) but also to prevent complement-mediated diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous complement protein conversion and deposition at a specific site (e.g. a virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application is eliminating any cancer cells left after surgical removal of a tumour). Also contemplated is ex vivo treatment, especially by passing blood through a matrix containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or wife-mismatched lymphocytes in extracted bone marrow. Since (A) is not inhibited by factor I, it can bind repeatedly to factor B (which is then
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07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (see AAW34606 for wild type protein). This protein is a protein of the invention, and is a modified native complement pathway protein (A) that forms a down-regulation resistant C3 convertase. (A), their variants,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IMUT-) IMUTRAN LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents a mutated human C3 protein of the invention AAW34606 for wild type protein). This protein is a protein of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TC,
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on, etc.
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96GB-0004865.
96GB-0011896.
96GB-0014293.
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1431
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RESULT 17
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This sequence represents a mutated human C3 protein of the invention (see ANW34606 for wild type protein). This protein is a protein of the invention, and is a modified native complement pathway protein (A) that forms a down-regulation resistant C3 convertase. (A), their variants, fragments and conjugates are used to deplete levels of complement pathway proteins (by superactivation until one or more complement (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign material (particularly a xenograft) but also to prevent complement-mediated disease, also to localise and/or amplify endogenous complement protein conversion and deposition at a specific site (e.g. a virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application is eliminating any cancer cells left after surgical removal of a tumour). Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-NOV-1996;
07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft rejection, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; C3 protein; convertase; complement pathway protein; infection; down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour; complement-mediated response; MHC-mismatched lymphocyte; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inactivated), causing inactivation consumption of factor B.
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96GB-0004865.
96GB-0011896.
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Pred. No.
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07-MAR-1996;
07-JUN-1996;
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                                                                                       Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft
                                                                                                                                          WPI; 1997-457534/42
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Misc-difference 1634
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                                                    Example 17; Page
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                                                                                                                                                                                                                                                                                                        12-SEP-1997.
This sequence represents a mutated human C3 protein of the invention (see AAW34606 for wild type protein). This protein is a protein of tinvention, and is a modified native complement pathway protein (A) tinvention, and
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ilarity 100.0%;
Conservative
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96GB-0004865.
96GB-0011896.
96GB-0014293.
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                                                   -; 123pp; English
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Pred. No. 0.0069;
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RESULT 19
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08-JUL-1996;
           Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft rejection, etc.
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96GB-0014293.
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1638..1645
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Pred. No. 0.0069;
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Example 17;

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Best Local (
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07-MAR-1996;
07-JUN-1996;
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               Farries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human C3 protein mutant R1303X, R1320X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW40988 standard; Protein; 1663 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                               (IMUT-) IMUTRAN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1307
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AAW34606
                                                                                                                                                                                                                                                                                                                                                                      sapiens
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               Harrison
                                                                            96GB-0004865.
96GB-0011896.
96GB-0014293.
                                                                                                                                   96GB-0024028
                                                                                                                                                                  97WO-GB00603
                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                 /label= Glu, Tyr, Cys, Trp, Gln, Gly
                                                                                                                                                                                                                                                                                                  /label= Glu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a mutated human C3 protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                  Tyr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 70; DB 18;
Pred. No. 0.0069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                    сув,
                                                                                                                                                                                                                                                                                              Trp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 18;
                                                                                                                                                                                                                                                                                                  Gln,
                                                                                                                                                                                                                                                                                                  Gly
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Sequence

1663 AA

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CC forms a down-regulation resistant C3 convertage. (A), their variants, CC fragments and conjugates are used to deplete levels of complement cpathway proteins (by superactivation until one or more components are cexhausted), specifically to prevent rejection of foreign material comparticularly a xenograft) but also to prevent complement-mediated complement grow (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous complement protein conversion and deposition at a specific site (e.g. a complement protein conversion and deposition at a specific site (e.g. a complement growed cell or tumour, to increase sensitivity to complement rediated responses; a particular application is eliminating contemplated is ex vivo treatment, especially by passing blood through a contemplated is ex vivo treatment, especially by passing blood through a contemplated is ex vivo treatment, especially by passing blood through a contemplated is ex vivo treatment, especially by passing blood through a contemplated by factor in (this may remove additional anabylactic peptides consumption of factor i, it can bind repeatedly to factor B, which is then can be consumption of factor B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft rejection, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page -; 123pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention, and is a modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents a mutated human C3 protein of the invention AAW34606 for wild type protein). This protein is a protein of the ntion, and is a modified native complement pathway protein (A) that is a down-regulation resistant C3 convertase. (A) their variants,
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                                                                                                                 Human C3 protein mutant R1303X
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                                                                                                                                                AAW40989 standard; Protein; 1663 AA.
                                                                                                                                                                                                    Local
                                                                                                                                                                           1307
                                                                                                                                                                                              l Similarity
13; Conserv
                                                                                                                                                                                    1 ITHRIHWESASLL 13
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                                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                                    Score 70; DB 18; Pred. No. 0.0069;
                                                                                                                                                                                               Mismatches
                                                                                                                                                                                               0;
                                                                                                                                                                                                         Length 1663;
                                                                                                                                                                                               Indels
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Human; C3 protein; convertase; complement pathway protein; infection; down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour; complement-mediated response; MHC-mismatched lymphocyte; mutein.

19-NOV-1996; 07-MAR-1996; 07-JUN-1996; 08-JUL-1996;

96GB-0004865. 96GB-0011896. 96GB-0014293. 96GB-0024028. 97WO-GB00603

04-MAR-1997;

12-SEP-1997 WO9732981-A1 Misc-difference

Location/Qualifiers /label= Glu, Gln, Gly

sapiens

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RESULT 22
AAW40990
   THE PROPERTY OF THE PROPERTY O
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                                  Misc-difference
                                                                                          Misc-difference
                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                           down-regulation resistant C3 convertage; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour; complement-mediated response; MHC-mismatched lymphocyte; mutein.
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                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human C3 protein mutant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; C3 protein; convertase; complement pathway protein; infection;
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                            /note= "D996S mutation" 997
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                                                                                                                                                                                                           Location/Qualifiers
                                                                                          996
                                                                                                                note= "D993A mutation"
note= "A997Q mutation"
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Pred. No. 0.0069;
                                                                                                                                                                               mutation"
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RESULT 23
AAW34606
ID AAW34

AAW34606 standard; Protein; 1663 AA

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                                                                                                                                 This sequence represents a mutated human C3 protein of the invention CC (see AAW34606 for wild type protein). This protein is a protein of the CC invention, and is a modified native complement pathway protein (A) that CC forms a down-regulation resistant C3 convertase. (A), their variants, CC fragments and conjugates are used to deplete levels of complement CC pathway proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign matterial CC (particularly a xenograft) but also to prevent complement-mediated CC diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous CC complement protein conversion and deposition at a specific site (e.g. a complement protein conversion and deposition at a specific site (e.g. a complement rediated responses; a particular application is eliminating CC contemplated is ex vivo treatment, especially by passing blood through a contemplated is ex vivo treatment, especially by passing blood through a cC contemplated is ex vivo treatment, especially by passing blood through a cC matrix containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or CC inhibited by factor I, it can bind repeatedly to factor B (which is then considered), causing inactivation of the alternative pathway by considered considered in activation of factor B (which is then considered considered in activation of the alternative pathway by
                                                                Matches
                                                                                               Query Match
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07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
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Misc-difference 1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft
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                                                                                                                                                                 consumption of factor B.
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1307
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13; Conserv
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ITHRIHWESASLL 1319
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96GB-0011896
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                                                              Score 70; DB 18;
Pred. No. 0.0069;
Mismatches 0
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                                                                                               18;
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                                                                                                                                                                               CC specifically to prevent rejection of foreign material (particularly a compound of foreign material) (particularly a compound of foreign material) (particularly a composition of foreign material) (particularly a composition in autoimmune composition) of composition in autoimmune composition and deposition at a specific site (e.g. a virus, infected cell conversion and deposition at a specific site (e.g. a virus, infected cell conversion and deposition at a specific site (e.g. a virus, infected cell conversion and deposition at a specific site (e.g. a virus, infected cell conversion and deposition at a specific site e.g. a virus, infected cell conversion and deposition at a specific site e.g. a virus, infected cell conversion and the sensitivity to complement-mediated responses; a conversion and application is eliminating any cancer cells left after conversion and the sensitivity of surgical removal of a tumour). Also contemplated is ex vivo treatment, conserved additional anaphylactic peptides and other inflammatory conserved by passing blood through a matrix containing (A) (this may conserved bone marrow. Since (A) is not inhibited by factor I, it can bind repeatedly to factor B (which is then inactivated), causing conserved the alternative pathway by consumption of factor B.
                                                                         Query Match
Best Local S
Matches 13
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07-MAR-1996;
07-JUN-1996;
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                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the wild type human C3 protein. This protein can be mutated to produce a protein of the invention. The protein of the invention is a modified native complement pathway protein (A) that forms a down-regulation resistant C3 convertase. (A), their variants, fragments and conjugates are used to deplete levels of complement pathway proteins (by superactivation until one or more components are exhausted).
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  1307
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                                                                           l Similarity
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ITHRIHWESASLL 1319
                                ITHRIHWESASLL
                                                                                                                                                    .1663
                                                                           Conservative
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96GB-0004865.
96GB-0011896.
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                                                                                         100.0%;
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                                                                                           Score 70; DB 18,
Pred. No. 0.0069,
                                                                                                                DB 18;
                                                                                                             Length 1663;
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                                                                       Gaps
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RESULT 24 AAW34607

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1 ITHRIHWESASLL 13

Query Match Best Local S Matches

Similarity

100.0%;

Score 70; DB 18; Pred. No. 0.0069; Mismatches

DB 18;

Length 1663; Indels

0

0

Conservative

0;

Sequence

1663 AA

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This sequence represents a mutated human C3 protein of the invention (see AAW34606 for wild type protein). This protein is a protein of the invention, and is a modified native complement pathway protein (A) that forms a down-regulation resistant C3 convertase. (A), their variants, fragments and conjugates are used to deplete levels of complement pathway proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign material (particularly a xenograft) but also to prevent complement-mediated diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous complement protein conversion and deposition at a specific site (e.g. a virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application is eliminating any cancer cells left after surgical removal of a tumour). Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-NOV-1996;
07-MAR-1996;
07-JUN-1996;
                                               contemplated is ex vivo treatment, especially by passing blood through a matrix containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or MHC-mismatched lymphocytes in extracted bone marrow. Since (A) is not inhibited by factor I, it can bind repeatedly to factor B (which is then inactivated), causing inactivation of the alternative pathway by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft rejection, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; C3 protein; convertase; complement pathway protein; infection; down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour; complement-mediated response; MHC-mismatched lymphocyte; mutein.
                                   consumption
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Page -; 123pp; English.
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                                   of factor
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96GB-0004865.
96GB-0011896.
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RESULT 25
AAW34608
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                                         This sequence represents a mutated human C3 protein of the invention CC (see AAW34606 for wild type protein). This protein is a protein of the CC invention, and is a modified native complement pathway protein (A) that CC forms a down-regulation resistant C3 convertase. (A), their variants, CC fragments and conjugates are used to deplete levels of complement CC pathway proteins (by superactivation until one or more components are CC exhausted), specifically to prevent rejection of foreign material CC (particularly a xenograft) but also to prevent complement-mediated CC diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous CC complement protein conversion and deposition at a specific site (e.g. a CC virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application is eliminating CC complement-mediated responses; a particular application is eliminating CC contemplated is ex vivo treatment, especially by passing blood through a CC matrix containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or CC inhibited by factor I, it can bind repeatedly to factor B (which is then considered in activated), causing inactivation of the alternative pathway by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft rejection, etc.
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08-JUL-1996;
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07-MAR-1996;
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96GB-0004865.
96GB-0011896.
96GB-0014293.
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Sequence

consumption

of factor

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AAW34609
ID AAW3
This sequence represents a mutated human C3 protein of the invention CC (see AAW34606 for wild type protein). This protein is a protein of the cinvention, and is a modified native complement pathway protein (A) that CC forms a down-regulation resistant C3 convertase. (A), their variants, cf fragments and conjugates are used to deplete levels of complement cC pathway proteins (by superactivation until one or more components are certaints, psecifically to prevent rejection of foreign material (particularly a xenograft) but also to prevent complement-mediated CC diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous cc virus, infected cell or tumour, to increase sensitivity to complement protein conversion and deposition at a specific site (e.g. a crimus, infected cell or tumour, to increase sensitivity to complement mediated responses; a particular application is eliminating CC contemplated is ex vivo treatment, especially by passing blood through a contemplated is ex vivo treatment, especially by passing blood through a contemplated is ex vivo treatment, especially by passing blood through a contemplated is ex vivo treatment, especially by passing blood through a contemplated is ex vivo treatment, especially by passing blood through a contemplated is ex vivo treatment, especially by passing blood through a contemplated is extracted bone marrow. Since (A) is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 13
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07-MAR-1996;
07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-APR-1998 (first entry)
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100.0%; Pred. No. 0.0069;
tive 0; Mismatches 0;
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RESULT 27
AAW34610
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Best Local
This sequence represents a mutated human C3 protein of the invention (see AAW34606 for wild type protein). This protein is a protein of the invention, and is a modified native complement pathway protein (A) that forms a down-regulation resistant C3 convertase. (A), their variants, fragments and conjugates are used to deplete levels of complement pathway proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign material (particularly a xenograft) but also to prevent complement-mediated diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous complement protein conversion and deposition at a specific site (e.g. a virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application is eliminating
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07-MAR-1996;
07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; C3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; convertase; complement pathway protein; infection;
lation resistant C3 convertase; xenograft rejection; therapy;
t-mediated disease; autoimmune disease; leukaemia cell; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by factor I, it can bind repeatedly to factor B (which is ed), causing inactivation of the alternative pathway by
                                                                                                                                                                                                                                                etc.
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RESULT 28
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                                                                                                                                                   Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft
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Pred. No. 0.0069;
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This sequence (see AAW34606

represents a mutated human C3 protein of the invention for wild type protein). This protein is a protein of the

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Matches 13
19-NOV-1996;
07-MAR-1996;
07-JUN-1996;
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Pred. No. 0.0069;
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RESULT 30
AAW34613
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                             Misc-difference
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            "V1005H mutation
                                                                              "K1001N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 70; DB 18;
Pred. No. 0.0069;
                                                                              mutation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                    infection;
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WO9732981-A1

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RESULT 31
AAW34614
ID AAW34
AC AAW34
AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC This sequence represents a mutated human C3 protein of the invention CC (see AAW34606 for wild type protein). This protein is a protein of the cinvention, and is a modified native complement pathway protein (A) that CC forms a down-regulation resistant C3 convertase. (A), their variants, CC fragments and conjugates are used to deplete levels of complement CC pathway proteins (by superactivation until one or more components are calcularly a xenograft) but also to prevent complement-mediated CC (particularly a xenograft) but also to prevent complement-mediated CC diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous CC complement protein conversion and deposition at a specific site (e.g. a CC virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application is eliminating CC contended is ex vivo treatment, especially by passing blood through a CC contended is ex vivo treatment, especially by passing blood through a CC matrix containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or inactivated by factor I, it can bind repeatedly to factor B (which is then inactivated), causing inactivation of the alternative pathway by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
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07-MAR-1996;
07-JUN-1996;
                                                         down-regulation resi
complement-mediated
complement-mediated
                                                                            Human; C3 protein; convertase; complement pathway protein; infection; down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour;
                                                                                                                                                                                                                                                                                09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complemen pathway by super-activation, especially for preventing graft rejection, etc.
      Homo sapiens
                                                                                                                                                                                                             Human C3 protein mutant DV-3.
                                                                                                                                                                                                                                                                                                                                          AAW34614;
                                                                                                                                                                                                                                                                                                                                                                                                   AAW34614 standard; Protein; 1663 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inactivated), causing consumption of factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    consumption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 14; Page -; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-457534/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Farries
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13; Conserv
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96GB-0011896
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                                                         response;
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Pred. No. 0.0069;
                                                         MHC-mismatched lymphocyte; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 18;
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RESULT 32 AAW34615 ID AAW34

AAW34615 standard; Protein; 1663 AA.

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                                                                                                                               This sequence represents a mutated human C3 protein of the invention CC (see AAM34606 for wild type protein). This protein is a protein of the convention, and is a modified native complement pathway protein (A) that CC invention, and is a modified native complement pathway protein (A) that CC forms a down-regulation resistant C3 convertase. (A) their variants, CC fragments and conjugates are used to deplete levels of complement pathway proteins (by superactivation until one or more components are cathway proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign material CC (particularly a xenograft) but also to prevent complement-mediated CC (particularly a xenograft) but also to prevent complement-mediated CC (complement protein conversion and deposition at a specific site (e.g. a CC complement protein conversion and deposition at a specific site (e.g. a CC complement protein conversion and deposition at a specific site (e.g. a CC complement calls left after surgical removal of a tumour). Also CC consequence calls left after surgical removal of a tumour). Also contemplated is ex vivo treatment, especially by passing blood through a matrix containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or CC consequence and contemplated is extended to extracted bone marrow. Since (A) is not inhibited by factor I, it can bind repeatedly to factor B (which is then constituted), causing inactivation of the alternative pathway by
                                                               Matches
                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-NOV-1996;
07-MAR-1996;
07-JUN-1996;
                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft rejection, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
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                                                                                                                                                           consumption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 14; Page -; 123pp; English
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                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TC,
                           ITHRIHWESASLL 13
                                                                                                                               1663 AA;
                                                                                                                                                              of factor
                                                               Conservative
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96GB-0011896.
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1033
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                                                                              Score 70;
Pred. No.
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                                                               Mismatches
                                                                              0.0069;
                                                                                               BB
                                                                                            Length 1663;
                                                               Indels
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                                                               Gaps
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19-NOV-1996;
07-MAR-1996;
07-JUN-1996;
                     virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application is eliminating any cancer cells left after surgical removal of a rumour). Also contemplated is ex vivo treatment, especially by passing blood through a matrix containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or MHC-mismatched lymphocytes in extracted bone marrow. Since (A) is not inhibited by factor I, it can bind repeatedly to factor B (which is then inactivated), causing inactivation of the alternative pathway by
                                                                                                                                                                                                                                                                                                                          fragments and conjugates are used to deplete levels of complement pathway proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign material (particularly a xenograft) but also to prevent complement-mediated diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous complement protein conversion and deposition at a specific site (e.g. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft rejection, etc.
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consumption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a mutated human C3 protein of the invention (see AAW34606 for wild type protein). This protein is a protein of the invention, and is a modified native complement pathway protein (A) that forms a down-regulation resistant C3 convertase. (A), their variants,
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of factor
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96GB-0004865.
96GB-0011896.
96GB-0014293.
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1072
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1073
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1071
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RESULT 33
AW34616
ID AW34
XX Human
XX Homo
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This sequence represents a mutated human C3 protein of the invention (see AAW34606 for wild type protein). This protein is a protein of the cinvention, and is a modified native complement pathway protein (A) that forms a down-regulation resistant C3 convertase. (A), their variants, cf fragments and conjugates are used to deplete levels of complement proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign material (particularly a xenograft) but also to prevent complement—mediated (diseases resulting from (surgical) injury or antibody-antigen interaction c1 in autoimmune disease, also to localise and/or amplify endogenous complement protein conversion and deposition at a specific site (e.g. a virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application is eliminating c2 contemplated is ex vivo treatment, especially by passing blood through a matrix containing (A) (this may remove additional anaphylactic peptides and other inflammatory mediators) or killing of leukaemia cells or other inflammatory mediators) or killing of leukaemia cells or
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified complement pathway protein that forms C3 convertase resistrant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft rejection, etc.
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07-JUN-1996;
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96GB-0011896.
96GB-0014293.
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100.0%; Pred. No. 0.0069;
tive 0; Mismatches 0;
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            This sequence represents a mutated human C3 protein of the invention (see AW34606 for wild type protein). This protein is a protein of the invention, and is a modified native complement pathway protein (A) that forms a down-regulation resistant C3 convertase. (A), their variants, fragments and conjugates are used to deplete levels of complement pathway proteins (by superactivation until one or more components are exhausted), specifically to prevent rejection of foreign material (particularly a xenograft) but also to prevent complement-mediated
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                                                                                                                            Claim 18; Page -; 123pp; English.
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          pecifically to prevent rejection of foreign material a xenograft) but also to prevent complement-mediated
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96GB-0014293.
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 (surgical)
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Pred. No. 0.0069;
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 injury or antibody-antigen interaction
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07-MAR-1996;
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                                                                                                                                                                                          Modified complement pathway protein that forms C3 convertase resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft rejection, etc.
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inactivated) factor
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Pred. No.
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This sequence represents a mutated human C3 protein of the invention (see AAW34606 for wild type protein). This protein is a protein of the invention, and is a modified native complement pathway protein (A) the invention, and is a modified native complement pathway protein (A) the invention of the invention of

123pp;

English

a down-regulation resistant C3 convertase.

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RESULT 36
AAW34626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC fragments and conjugates are used to deplete levels of complement CC pathway proteins (by superactivation until one or more components are CC exhausted), specifically to prevent rejection of foreign material CC (particularly a xenograft) but also to prevent complement endiated CC diseases resulting from (surgical) injury or antibody-antigen interaction CC in autoimmune disease, also to localise and/or amplify endogenous CC complement protein conversion and deposition at a specific site (e.g. a virus, infected cell or tumour, to increase sensitivity to CC complement-mediated responses, a particular application is eliminating CC contemplated is ex vivo treatment, especially by passing blood through a CC contemplated is ex vivo treatment, especially by passing blood through a CC matrix containing (A) (this may remove additional anaphylactic peptides CC and other inflammatory mediators) or killing of leukaemia cells or CC minibited by factor I, it can bind repeatedly to factor B (which is then CC inactivated), causing mactivation of the alternative pathway by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                            19-NOV-1996;
07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; C3 protein; convertase; complement pathway protein; infection; down-regulation resistant C3 convertase; xenograft rejection; therapy; complement-mediated disease; autoimmune disease; leukaemia cell; tumour; complement-mediated response; MHC-mismatched lymphocyte; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW34626 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        consumption of factor B.
 Example 17; Page -; 123pp; English
                                              pathway by super-activation,
                                                           Modified complement pathway protein that forms C3 convertage resistant to down-regulation - used to exhaust the complement
                                                                                                               WPI; 1997-457534/42
                                                                                                                                              Farries TC,
                                                                                                                                                                                                                                                                                            04-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                           W09732981-A1
                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                              (IMUT-) IMUTRAN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1307 ITHRIHWESASLL 1319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein mutant FT-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITHRIHWESASLL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1663 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                              Harrison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                          96GB-0024028.
96GB-0004865.
96GB-0011896.
96GB-0014293.
                                                                                                                                                                                                                                                                                            97WO-GB00603
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1621..1625
                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein; 1667 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                       "wild type residues IIGKD mutated to RYIYPLDSL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           o
;
                                                especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 70; DB 18;
Pred. No. 0.0069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>,</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                 19-NOV-1996;
07-MAR-1996;
07-JUN-1996;
08-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a mutated human C3 protein of the invention (see AAW34606 for wild type protein). This protein is a protein of the invention, and is a modified native complement pathway protein (A) their variants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; C3 protein; convertase; complement pathway protein; infectiown-regulation resistant C3 convertase; xenograft rejection; tocomplement-mediated disease; autoimmune disease; leukaenia cell; complement-mediated response; MHC-mismatched lymphocyte; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human C3 protein mutant FR-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW34631 standard; Protein; 1667 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
Modified complement pathway protein that forms
                                                              WPI; 1997-457534/42
                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9732981-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ITHRIHWESASLL 13
                                                                                                                                'n,
                                                                                                                                                                                                   IMUTRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITHRIHWESASLL 1319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                Harrison RA;
                                                                                                                                                                                                                                                                                                    96GB-0024028.
96GB-0004865.
96GB-0011896.
                                                                                                                                                                                                                                                                     96GB-0014293
                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-GB00603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "wild type D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 70; DB 18;
Pred. No. 0.0069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutated to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This protein is a protein of the omplement pathway protein (A) that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
   C3 convertase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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CC This sequence represents a mutated human C3 protein of the invention (see AAW34606 for wild type protein). This protein is a protein of the cinvention, and is a modified native complement pathway protein (A) that CC forms a down-regulation resistant C3 convertase. (A), their variants, CC pathway proteins (by superactivation until one or more components are can pathway proteins (by superactivation until one or more components are can pathway proteins (by superactivation until one or more components are comparated and comparated protein protein protein protein conversion and deposition of foreign material c3 diseases resulting from (surgical) injury or antibody-antigen interaction in autoimmune disease, also to localise and/or amplify endogenous complement protein conversion and deposition at a specific site (e.g. a virus, infected cell or tumour, to increase sensitivity to complement-mediated responses; a particular application; Also complement cells left after surgical removal of a tumour). Also contemplated is ex vivo treatment, especially by passing blood through a can can certification of the analyticatic peptides cand other inflammatory mediators) or killing of leukaemia cells or c4 inhibited by factor I, it can bind repeatedly to factor B (which is then can sumption of factor B.
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                           Human; complement; C3f; SELDI; myocardial infarction; surface enhanced laser description ionisation; intracerebral haemorrhage; congestive heart failure; mass spectroscopy; immunoassay; radioimmunoassay; enzyme-linked immunosorbent assay; ELISA;
                                                             (MARS/)
(YANT/)
                                                                                                                                                                                                                                                                                                                                                                                         Human complement C3f derived peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
              Jackowski G,
                                                                                                                                      30-APR-2001; 2001US-0845715
                                                                                                                                                                     30-APR-2001; 2001US-0845715.
                                                                                                                                                                                                                                  US2002161184-A1
                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                              fluorescent immunoassay.
                                                                                                                                                                                                                                                                                                                                                                                                                         10-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU08967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU08967 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resistant to down-regulation - used to exhaust the complement pathway by super-activation, especially for preventing graft rejection, etc.
                                                                                                         (JACK/) JACKOWSKI G.
                                                                                          (THAT/)
                                              VREE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1307
                                                           THATCHER B.
MARSHALL J.
YANTHA J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              بر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
                                              VREES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITHRIHWESASLL 1319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITHRIHWESASLL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                              7
            Thatcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -; 123pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
              Β,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
              Marshall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 70; DB 18;
Pred. No. 0.0069;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
              Yantha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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RESULT 39
ABG72971
ID ABG72
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a biopolymer marker comprises a compliment C3f fragment appearing as ABU08967 having a molecular weight of 1348 dalcons. The fragment was isolated from samples from affected individuals using SELDI (surface enhanced laser desorption ionisation) and a protein chip. The marker is useful in methods for diagnosing a disease state such as myocardial infarction, intracerebral hemorrhage or congestive heart failure. The methods used include mass spectroscopy or immunoassays, e.g. radioimmunoassay, enzyme-linked immunosorbent assay (ELISA) or fluorescent immunoassays. The invention enables a diagnostician to characterise the presence or absence of the disease state relative to recognition of the presence or absence of the biopolymer, respectively. The presence is the human complement C3f derived peptide of the biopolymer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biopolymer marker, useful in diagnosing disease states including myocardial infarction and intracerebral hemorrhage, comprises compliment C3f fragment with a specified molecular weight -
                           New biopolymer markers useful for indicating one particular disease state such as myocardial infarction, congestive heart failure and intracerebral hemorrhage
                                                                                                                                                                                                                                                                                                                                                                                                            Human; biopolymer marker;
congestive heart failure;
Claim 1; Page 30; 30pp; English
                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human complement C3f fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                       WPI; 2003-111908/10.
                                                                                                                 Jackowski G,
                                                                                                                                                                          30-APR-2001; 2001US-0845731.
                                                                                                                                                                                                      29-APR-2002; 2002WO-CA00632.
                                                                                                                                                                                                                                    07-NOV-2002.
                                                                                                                                                                                                                                                               WO200288731-A2
                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG72971 standard; Peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 7; 11pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-340874/32
                                                                                                                                              (SYNX-) SYN.X PHARMA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention.
                                                                                                                                                                                                                                                                                                                                                                               sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA
;
                                                                                                               Thatcher B,
                                                                                                                                                                                                                                                                                                           /note= "His is optionally absent"
12
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                         /note= "Arg is optionally absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.1%;
                                                                                                                                                                                                                                                                                                                                                                                                          myocardial infarction; C3f; syndrome > intracerebral haemorrhage; complement.
                                                                                                                  Marshall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>,</u>
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Pred. No.
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                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventice useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB0737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic a genes from Drosophila interactions -
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reation, but was obtained in electronic format directly from .wipo.int/pub/published_pct_sequences.
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US-09-449-218D-43
US-09-668-529A-43
US-09-668-529A-43
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ALIGNMENTS	US-08-632-434-2	US-08-632-434-6	US-08-632-434-8	US-09-252-991A-32422	US-09-252-991A-28140	US-09-252-991A-19372	US-08-729-103-4	US-09-107-532A-3813	US-08-889-013C-6	US-09-491-522-5	US-09-491-522-11	US-09-252-991A-26112	US-09-107-532A-7065	US-09-252-991A-18995	US-09-491-522-7	US-09-040-444-1	US-08-501-572-1	US-09-252-991A-31968	
		ტ.	Sequence 8, Appli	Sequence 32422, A	Sequence 28140, A	Sequence 19372, A	Sequence 4, Appli	Sequence 3813, Ap	Sequence 6, Appli	Sequence 5, Appli	Sequence 11, Appl	Sequence 26112, A	Sequence 7065, Ap	Sequence 18995, A	Sequence 7, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 31968, A	

; MOLECULE TYPE: protein US-08-793-126-1 RESULT 1 US-08-793-126-1 Query Match Best Local Similarity Matches 13; Conserv Sequence 1, Application US/08793126 Patent No. 5849297 GENERAL INFORMATION: TELEFAX: (617) 526-500 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: ATTORNEY/AGENT INFORMATION: NAME: Baker, Hollie L. REGISTRATION NUMBER: 31,321 REFERENCE/DOCKET NUMBER: 1022 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 526-6000 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, 'CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/793,126 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy CORRESPONDENCE ADDRESS: ADDRESSEE: HALE AND DORR LLP APPLICANT: Farries, Charles Timothy TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS APPLICANT: Harrison, Richard Alexander APPLICANT: Farries, Charles Timothy NUMBER OF SEQUENCES: TYPE: amino acid STRANDEDNESS: sir TOPOLOGY: linear FILING DATE: 07-FEB-1997 CLASSIFICATION: 424 LENGTH: CITY: Boston STREET: 02109 1663 amino acids 60 State Street United States of America Floppy disk single 526-5000 100.0%; 102286.377 Score 70; DB 2; 1 Pred. No. 0.0036; ; Mismatches 0; Version #1 Length 1663;

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                                                                      SOFTWARE: Patentin
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        Patent No.
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APPLICANT: Harrison, Richard Alexander
APPLICANT: Farries, Charles Timothy
TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS
                                                                                                            EARLIER APPLICATION NUMBER: PCT/GB97/00603
EARLIER FILING DATE: 1997-03-04
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/142,334
CURRENT FILING DATE: 1999-04-15
                                                                                                                                                                                                      APPLICANT: Farries, Timothy C.
APPLICANT: Harrison, Richard A.
TITLE OF INVENTION: Down-Regulation Resistant
FILE REFERENCE: 4-30443/A/IMU/PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 526-6000
TELEPAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1663 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07-FEB-1997
ATTORNEY AGENT INFORMATION:
NAME: Baker; HOllie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 1022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
               TYPE: PRT
ORGANISM: Homo sapiens
                                                      LENGTH: 1663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/132,271 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                        1307
                                                                                                                                                                                                                                                                                                        22, Application US/09142334
o. 6268485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; ilarity 100.0%; Conservative 0;
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                                                                                              Ver.
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22644
LENGTH: 281
片
                                                                                                                                                US-09-252-991A-21635
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US-09-252-991A-22644
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                                                                                                                                                                                                    SEQ ID NO 21635
LENGTH: 280
                                                                         Matches
                                                                                        Query Match
Best Local
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APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21635, Application US/09252991A Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                             APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                             TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.7%;
Local Similarity 58.3%;
es 7; Conservation
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121
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                                  1 ITHRIHWESASLL 13
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                                                                       Similarity 6; Conserv
IVHRLDWETSGLM 133
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                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09252991A
                                                                                      60.0%;
46.2%;
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Pred. No. 4.2;
                                                                                      Score 42; DB
Pred. No. 18;
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                                                                         Mismatches
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                                                                                                       Length 280;
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                                                                       Indels
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RESULT 6

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FILE REFERENCE: 107196.136
FULE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24616
LENGTH: 221
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. boomation:
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Best Local
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                    INFORMATION FOR SEQ ID NO: 5290: SEQUENCE CHARACTERISTICS: LENGTH: 264 amino acids
                                                                                                                                                                                                                                                      FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                      NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: CD/RC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                TOPOLOGY: linear MOLECULE TYPE: protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 7310
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8; Conserv
                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 100 Beaver Street
                                                                                                                                       TELEFAX:
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YES
                                                                                                                                   (781)893-8277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
43;
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                                                                                                                                          US-09-107-532A-7038
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US-09-107-532A-7038
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PATENT NO. 6583275
PATENT NO. 6583276
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT A Doucette-Stamm and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: JULY 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 7038:
   Matches
                                                                     Query Match
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Local Similarity tes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...329
SEQUENCE DESCRIPTION: SEQ ID NO: 7038:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...264
SEQUENCE DESCRIPTION: SEQ ID NO: 5290:
                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7038,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ITHRI--HWESASLL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          038, Application US/09107532A
6583275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
                                                                                                                                                                                                                                                                                                               ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: GENOME THERAPEUTICS CORPORATION
   Conservative
                                    55.7%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                     protein
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   4; Mismatches
                                        Score 39; DB Pred. No. 65;
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                                                                     DB
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                                                                     Length 329;
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   Gaps
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                                                                                                                             US-09-668-529A-43
                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/668,529A
CURRENT FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 43
LENGTH: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 43
LENGTH: 267
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 43,
                                                            Best Local Similarity
Matches 4; Conserv
                                                                                           Query Match
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APPLICANT:
                                                                                                                                                                                                                                                                    APPLICANT: Van Ness, Jeffrey
APPLICANT: Winkler, David G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING BONE
TITLE OF INVENTION: MINERALIZATION
FILE REFERENCE: 240083.508D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/449,218D CURRENT FILING DATE: 1999-11-24 NUMBER OF SEQ ID NOS: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Van Ness, Jeffrey
APPLICANT: Winkler, David G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
TITLE OF INVENTION: BONE MINERALIZATION
FILE REFERENCE: 240083.508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Brunkow, Mary E. APPLICANT: Galas, David J.
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Brunkow, Mary E. APPLICANT: Galas, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.
 154
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o. 6395511
                              2 THRIHWES 9
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Mulligan, John T.
Paeper, Bryan W.
Van Ness, Jeffrey
SHEVHWET 161
                                                                                                                                                                                                                                                                                                                                                                   Kovacevich, Brian
Mulligan, John T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09668529A
                                                                                                                                                                                                                                                                                                                                                    Paeper, Bryan W.
                                                             Conservative
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                                                                            Score 37; DB 4;
Pred. No. 1.1e+02;
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                                                             Mismatches
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1.1e+02;
                                                                                           Length 267;
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RESULT 11

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Sequence 43, Application US/09668037A
Patent No. 6495736
GENERAL INFORMATION:
APPLICANT: Brunkow, Mary E.
APPLICANT: Galas, David J.
APPLICANT: Kovacevich, Brian
APPLICANT: Mulligan, John T.
APPLICANT: Mulligan, John T.
APPLICANT: Paeper, Bryan W.
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US-08-887-997B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-668-037A-43
US-08-887-997B-2
                                                                                                                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,997B
FILING DATE: 03-UUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, STEVEN R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI 5290
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
TELEPHONE: (617) 498-8260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/668,037A
CURRENT APPLICATION NUMBER: US/09/668,037A
CURRENT FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 45
SOFTWARE: RastSEQ for Windows Version 3.0
SEQ ID NO 43
LENGTH: 267
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                                                                      TELEPHONE: (617) 498-8260
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: FOLLET
APPLICANT: DEROBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Van Ness, Jeffrey
APPLICANT: Winkler, David G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING BONE
TITLE OF INVENTION: MINERALIZATION
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                    TOPOLOGY: 1:--
TOPOLOGY: 1:--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cambridge
STATE: Marridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
es 4; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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5. 5935852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 THRIHWES 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOLLETTIE, MAXIMILLIAN DEROBERTIS, EDWARD M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IS, EDWARD M.
Mammalian Cerberus-Like Protein &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
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Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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RESULT 14
US-08-311-731A-71
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US-08-311-731A-291
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                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Mycobacterium leprae
US-08-311-731A-291
                                                      Sequence 71, Application US/08311731A
Patent No. 6582366
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 291, Application US/08311731A Patent No. 6583266
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SMITH, DUBLET APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID S
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUE
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,6
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                              Match 52.9%;
Local Similarity 50.0%;
es 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
                                                                                                                                                                                           | :|| :|:|
165 HLVHWATANL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 SHEVHWET 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         526 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             617/720-3500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MYCOBACTERIUM TUBERCULOSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C0044/7125
                                                                                                                                                                                                                                                            Score 37; DB 4; Le
Pred. No. 2.2e+02;
3; Mismatches 2;
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1.1e+02;
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US-09-413-814-68
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APPLICANT: Mueller, Joachim
APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT APPLICATION NUMBER: DE 198 46 493.2
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER APPLICATION NUMBER: DE 198 46 493.2
SARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
LENGTH: 700
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                   APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cino, Paul M
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bloecker, HelmappLICANT: Brandt, Petra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 617/720-3500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: WOLF, GRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 538 amino acids TYPE: amino acid TOPOLOGY: linear
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Pred. No. 2.2e+02;
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RESULT 17
US-09-066-262-3
; Sequence 3, Application US/09066262
; Patent No. 5965706
; GENERAL INFORMATION:
                                                                                                                                                     Query Match
Best Local Similarity
""" hes 5; Conserve
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Best Local Similarity
Forches 6; Conserv
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASSEG for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,710
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
EFFECTIVE TO THE PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELECHIONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hilman, Jennifer L.
APPLICANT: Goli, Surya K.
APPLICANT: Streeter, David G.
TITLE OF INVENTION: NEW REGULATOR
TITLE OF INVENTION: TRANSCRIPTION
                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 202344
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
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CITY: Palo Alto
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                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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5776698
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Pred. No. 2.
                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                    Score 36;
Pred. No.
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   ZIP: 94304
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RESULT 18
US-08-959-004-10
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                                                                                                                                                                                                                                                        Sequence 10, Application US/08959004 Patent No. 6197543 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/839,710
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
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APPLICANT: Streeter, David G.
TITLE OF INVENTION: NEW REGULATOR OF GENE
TITLE OF INVENTION: TRANSCRIPTION
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MEDIUM TYPE: Diskett
                                                                                   NUMBER OF SEQUENCES: 1
                                                                                                                   APPLICANT: Shah, Purvi
APPLICANT: Kaser, Matthew
TITLE OF INVENTION: HUMAN VESICLE MEMBRANE PROTEIN-LIKE
TITLE OF INVENTION: PROTEINS
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LIBRARY: GELL
ONE: 202344
STATE: C
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CITY: Palo Alto
STATE: CA
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                                                 ADDRESSEE: Incyte Pharmace
STREET: 3174 Porter Drive
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                                 CITY: Palo Alto
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 USA
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Corley, Neil C.
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                                                                     Incyte Pharmaceuticals, Inc
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RESULT 19
US-07-646-537B-2
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US-08-959-004-10
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: 625 amino acid
TELEFAX: (609) 921-4526 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GAUL, Timochy J.
REGISTRATION NUMBER: 33,111
REFERENCE/DOCKET NUMBER: DC1(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 921-5901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FASTERO for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/959,004 FILING DATE: Herewith CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Barbaci
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LIBRARY: GenBa
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                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 08543-4000
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Brist
STREET: P.O. Box
CITY: Princeton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 TYSVHWEESDI 244
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                                                                                                                                                                                                                                                                                                                     New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : GenBank
1665777
                                                                                                                                                                                                                                                                                                                                               P.O. Box 4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        625 amino acids
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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3.7e+02;
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US-08-299-567-5
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Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Applic
Patent No. 5747033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local 9
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APPLICANT: Mbamalu, Geraldine
APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYKOSINE KINASES
FILE REFERENCE: 11757.23USWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/214,631
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: PCT/CA97/00473
EARLIER FILING DATE: 1997-07-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 60/021,272
EARLIER FILING DATE: 1996-07-05
                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Davis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 13
                 COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATING
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                 APPLICANT: Davis, et al.
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                             STREET: 777 Old
CITY: Tarrytown
STATE: New York
  APPLICATION NUMBER:
                                                                                                                                                                                                                       ADDRESSEE: Regeneron Pharmaceuticals, Inc
STREET: 777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 844 amino acids
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us/08/299,567
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Pred. No. 2e+02;
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Pred. No. 5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 233;
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Sequence
Patent No. 551662.

Patent No. 551662.

PAPLICANT: BECKMANN, M. P.

APPLICANT: CERRETTI, DOUGLAS P.

APPLICANT OF INVESTION: CYTOKINE THAT BI
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REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG.

TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEPHONE: 914-345-7721
TINFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
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                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                 TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDITUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
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ADDRESSEE: IMMUNEX CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                   SEQUENCE CHARACTERISTICS:
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NAME: Kempler, Gail M.
                                                      TELEPHONE: (200) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%;
Local Similarity 57.1%;
Nes 4; Conservative
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TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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238 amino acids
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Pred. No.
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Query Match
Best Local Similarity
Watches 4; Conserve
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                                                                                                US-08-453-943-2
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GENERAL INFORMATION:
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Best Local S
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FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,943
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CERRETTI, DOUGLAS P. TITLE OF INVENTION: CYTOKINE THAT TITLE OF INVENTION: RECEPTOR HEK
                                                                                                                                                                                                                                         TELEPHONE: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: IMMUNEX CORPORATION STREET: 51 UNIVERSITY STREET CITY: SEATTLE
                                                                                                                                                                                                                                     TELEX: 756822
                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                 NAME: SEESE, KATHRYN A. REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 THNLHWK 157
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                                                                                                                                                     amino acid
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                                                                                                                                                                         238 amino acids
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                    Conservative
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                                    50.0%;
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                  Score 35; DB 1;
Pred. No. 2e+02;
2; Mismatches
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Pred. No. 2e+02;
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                                                           DB 1;
                    1.
                                                         Length 238;
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THRIHWE 8

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151

THNLHWK 157

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US-09-358-734-2
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TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TVPE: amino acid
TVPE: inino acid
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US-09-057-121-2
                                                                                                                 RESULT 25
                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-09-057-121-2
                                                                Sequence 2, Application US/09358734
Patent No. 6274117
                                                                                                                                                                                                                                  Matches
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Best Local Similarity
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                                                  GENERAL INFORMATION:
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APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:

ANALY. CEREC LATTORNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Microsoft Word for Apple, Version 5.1a CURRENT APPLICATION DATA:
APPLICATION DATA:
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Sy
                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
TITLE OF INVENTION: RECEPTOR HEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BECKMANN, APPLICANT: CERRETTI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 03-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                                                                                                                                                  151 THNLHWK 157
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                    BECKMANN,
CERRETTI,
                                                                                                                                                                                                                                Conservative
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, M. P.
, DOUGLAS P.
CYTOKINE THAT BINDS THE CELL SURFACE
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                                                                                                                                                                                                                                               Score 35; DB 2;
Pred. No. 2e+02;
                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                              Length 238;
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; TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3977
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US-09-134-001C-3977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-358-734-2
                                                         NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3977
LENGTH: 332
                                                                                                                                                                                                                                                                                                                         Sequence 3977, Applic Patent No. 6380370 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: DEPLEMENT OF DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 756822
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME: SEESE, KATHRIN ... 12

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2814

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1970-0430

TOT EDHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION:
FILING DATE: 20-ACCITION:
ATTORNEY/AGENT INFORMATION:
SEESE, KATHRYN A.
32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/358,734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/109,745 FILING DATE: 20-AUG-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28288
LENGTH: 356
TYPER: DATE
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                                                                                                                                                          US-09-252-991A-31968
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                                                                                                                                                                                               SEQ ID NO 31968
LENGTH: 542
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31968, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
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Best Local
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GENERAL INFORMATION:
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Best Local Similarity
Matches 7; Conserv
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                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                    APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 50.0%;
Local Similarity 85.7%;
les 6; Conservative
                                                                                              Local Similarity
236 HRLHWAAGQV 245
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                                     3 HRIHWESASL 12
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                                                                              Conservative
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Pred. No.
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Pred. No. 3.1e+02;
                                                                                              Score 35;
Pred. No.
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                                                                              Mismatches
                                                                                              DB 4;
4.7e+02;
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                                                                                                                 Length 542;
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RESULT

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RESULT 30
US-09-040-444-1
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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Koepsell, Hermann
APPLICANT: Grundeman, Dirk
APPLICANT: Grundeman, Dirk
APPLICANT: Gorboulev, Valentin
TITLE OF INVENTION: Transport protein Which Effects The
TITLE OF INVENTION: Transport Of Cationic Xenobiotics and\or Pharmaceuticals,
TITLE OF INVENTION: DNA Sequences Encoding It And Their Use.
                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202)408-4000
TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: TOOTHEY, Kimberlin M
REGISTRATION NUMBER: 35,391
REFERENCE/DOCKET NUMBER: 0246
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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APPLICANT: Grundeman, Dirk
APPLICANT: Koepsell, Hermann
I
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                       NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1300 I St
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                      STATE:
                                                                                                        CITY: Washington
                                                                                                                                ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner, STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner STREET: 1300 I Street, N.W., Suite 700
                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         424 IPHELHWLNVTL 435
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                                                                                                                                                                                                                                                                                                                                                                                 1, Application US/09040444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                      D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITHRIHWESASL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08501572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              556 amino acids
                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transport protein Which Effects The Transport Of Cationic Xenobiotics and\or Pharmaceuticals, DNA Sequences Encoding It And Their Use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02481.1453-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB 3;
Pred. No. 4.8e+02;
3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 556;
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OPERATING SYSTEM:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application Patent No. 6428998
GENERAL INFORMATION:
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Colige, Art. APPLICANT: Lapiere, Charles M. APPLICANT: Lapiere, Charles M. APPLICANT: Prockop, Darwin J. APPLICANT: PROCKOP, ORDER TITLE OF INVENTION: RECOMBINANT N-PROTEINASE, TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF ORDITION ORDITIONS: 17
                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Abrame, Samuel B
REGISTRATION NUMBER: 30,605
REPERENCE/DOCKET NUMBER: 8389-0060-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                       TELEPHONE: 650-493-5556
                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: O'Connor, Steven P
REGISTRATION NUMBER: 41,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 İPHELHWLNVTL 435
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    556 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                  Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMBER: US/09/040,444
March 18, 1998
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US-09-107-532A-7065
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US-09-252-991A-18995
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                                                                                                                                                                                                                                                                                                                                      Sequence 7065, Application.
Sequence 7065, Application.
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
APPLICANT: Lynn A DOUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: Marc J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%;
Local Similarity 55.6%;
tes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION UMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
                                                                                                      COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTMARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                           ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 HRVHW 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 HRIHW 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                             STATE: Massachusetts
                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                  CITY: Waltham
                                                                                                                                                                                                                                                                                 STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rubenfield et al.

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   452
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                                                                                                                                                                             CD/ROM ISO9660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 4;
Pred. No. 5.1e+02;
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Pred. No. 4.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                     and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 566;
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PRIOR APPLICATION NUMBER: US 60.
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26112
LENGTH: 860
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature;
LOCATION: (B) LOCATION 1...796;
SEQUENCE DESCRIPTION: SEQ ID NO: 7065;
US-09-107-532A-7065
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                                                                                                                                                                                                    RESULT 35
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                                                                                                                          Sequence 11, Application Patent No. 6428998
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 26112, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                             -09-252-991A-26112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILLING DATE: 1999-02-18
APPLICANT: Colige, A.......
APPLICANT: Lapiere, Charles M.
APPLICANT: Prockop, Darwin J.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 7065:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-01

TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113
                                                                                                                                                                                                                                                      93 LTHRLSFKQASL 104
                                                                                                                                                                                                                                                                                       1 ITHRIHWESASL 12
                                                                                                                                                                                                                                                                                                                       Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THRIHWES 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 796 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: July 2, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                Application US/09491522
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                                                                                                                                                                                                                                                                                                                         Conservative
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Pred. No. 6.9e
0; Mismatches
                                                                                                                                                                                                                                                                                                                       Score 35; DB
Pred. No. 7.4e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTC-012
                                                                                                                                                                                                                                                                                                                  7.4e+02;
2;
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                                                                                                                                                                                                                                                                                                                                                       Length 860;
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US-09-491-522-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1205 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Applic
Patent No. 6428998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
         COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASESEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                          APPLICANT: Colige, Alain
APPLICANT: Lapiere, Charles M.
APPLICANT: Prockop, Darwin J.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF
                                                                                                                                      COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION NUMBER: (
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                     STREET: 1155 Av
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1155 AV CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           438 HRFHWSRCS 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09491522
                                                                                                                                                                                                                                                          1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                             Pennie & Edmonds, LLP
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Pred. No. 1e+03;
0; Mismatches
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APPLICATION NUMBER:

08/886,333

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RESULT 37
US-08-889-013C-6
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Best Local Similarity 55.6%;
Matches 5; Conservative
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                              TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 105 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FI 930413
FILING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: CRAWFORD, ARTHUR R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 227-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
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                                 TOPOLOGY: unknown MOLECULE TYPE: protein FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Volume Telease #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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APPLICANT: FINNE, JUKKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1100 NO. CITY: ARLINGTON STATE: VIRGINIA
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REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A. ZIP: 22201-4714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1211 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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Streptococcus suis
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, Samuel B
30,605
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Pred. No. 1e+03;
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                                                                                                                           RESULT 38
US-09-107-532A-3813
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                                                              Matches
                                                                                            Query Match
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GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                                                           TELEPHONE: (781)893-5007
TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3813:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                             Local Similarity
                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
93
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                              6 HWESASLL 13
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HWETTSVL 100
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COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 100 Beaver Street
                                                                                                                                                                                                          ORGANISM: Enterococcus. faecium
                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                          ENGTH: 126 amino acids
                                                              Conservative
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                                                                             48.6%;
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57.1%;
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                                                                             Score 34; DB 4;
Pred. No. 1.5e+02;
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Pred. No. 1.3e+02
                                                              Mismatches
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                            1; Indels
                                                                                            Length 126;
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RESULT 39 US-08-729-103-4

Sequence 4, Application US/08729103 Patent No. 5837841

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LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
ILIBRARY: GenBank
CLONE: 474306
US-08-729-103-4
                                                                                                                                                                                                                                                                                                                                                                     US-09-252-991A-19372; Sequence 19372, Application US/09252991A; Patent No. 6551795
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PILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
BILING DATE:
NAME: BILLINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0138 US
TELEPHONE: 415-855-0555
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
                                      APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPBUTICS

FILE REPERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NO 19372

LENGTH: 226

TYPE: NEW CONTROL OF SEQ ID NOS: 33142

TYPE: NEW CONTROL OF SEQ ID NOS: 33142

LENGTH: 226
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Best Local Similarity 60.0%;
Matches 6; Conservative
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APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN REG PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
ORGANISM: Pseudomonas aeruginosa
                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3174 POI
CITY: Palo Alto
STATE: CA
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3174 Porter Drive
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Pred. No. 2e+02;
1; Mismatches
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US-09-252-991A-19372

Query Match
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps

Qy 3 HRIHW 7
||:||
Db 18 HRIHW 22
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Search completed: August 28, 2003, 14:14:56 Job time : 30 secs

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Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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seq length: 2000000000
                Match
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                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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'cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
'cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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2 6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
2 6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
2 6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
2 6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2 6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2 6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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US-09-875-519A-22
1 US-09-842-758-41
0 US-09-846-349-1
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US-09-845-731-1

US-09-842-758-42

US-10-183-116-45

US-10-183-116-47
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                          US-10-156-761-12347
US-10-074-475-209
US-10-183-116-79
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US-09-846-345-1
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31.196 Million cell updates/sec
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Sequence 1, Appli
Sequence 1, Appli
Sequence 22, Appl
Sequence 21, Appli
Sequence 41, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 42, Appli
Sequence 47, Appli
Sequence 47, Appli
Sequence 209, Appli
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US-10-014-070-5	US-09-815-242-11758	-09-374	US-10-270-333-75	-09-938-330-	US-09-938-330-2	-10-255-969-	US-10-139-262-4	55-	9-262-	US-10-103-313-541	US-10-103-313-418	US-09-764-891-4103	US-10-255-969-2	-10-139-	-10-097-340-	US-10-106-698-4945	US-09-089-818B-2	-09-887-552A	÷	-10-286-152A-	-10-139-814-1	US-09-089-818B-8	US-10-002-631C-135	US-09-864-761-46114	US-09-864-761-34487	US-09-864-761-44965	35	US-09-800-198-57	US-09-808-602-68
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ALIGNMENTS

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US-09-846-345-1
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Sequence 1, Application US/09846345
Patent No. US20020161182A1
GENERAL INFORMATION:
APPLICANT: Jackowski, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE
TITLE OF INVENTION: OF 1865 DALTONS
FILE REFERENCE: 2132.045
CURRENT APPLICATION NUMBER: US/09/846,345
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Matches
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APPLICANT: Jackowski, George
APPLICANT: Jackowski, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
TITLE OF INVENTION: OF 1690 DALITONS
FILE REFERENCE: 2132.042
CURRENT APPLICATION NUMBER: US/09/845,730
CURRENT FILING DATE: 2001-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09845730 Patent No. US20020169278A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 14
                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                Similarity
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Pred. No. 7.3e-05;
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                                                               OF DISEASE STATE HAVING A MOLECULAR
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; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-846-346-1
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                                                                                                                                                                       PRIOR APPLICATION NUMBER: 2001-06-06
PRIOR PILING DATE: 1997-03-04
NUMBER OF SEQ ID NOS: 35
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH.
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NUMBER OF SEQ ID NOS: 1
SOFTWARE: PATENTIN VERSION
SEQ ID NO 1
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Best Local Similarity
Matches 13; Conserv
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                                                                Query Match
Best Local (
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Best Local Similarity
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CURRENT FILING DATE: 2001-04-30
NUMBER OF SEO ID NOS: 1
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                    APPLICANT: Farries, Timothy C. APPLICANT: Harrison, Richard A. TITLE OF INVENTION: Down-Regulation Resistant FILE REFERENCE: 4-30443/A/IMU/PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jackowski, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
TITLE OF INVENTION: OF 1998 DALTONS
FILE REFERENCE: 2132.013
                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/875,519A CURRENT FILING DATE: 2001-06-06
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                     ENGTH: 1663
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1 ITHRIHWESASLL 13
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                                                                Similarity
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                                                  Conservative
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                                                                100.0%;
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                                             Score 70; DB y; L
Pred. No. 0.0063;
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; ORGĀNISM: Homo sapiens
US-09-842-758-41
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CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/200,158
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 2000-04-26
PRIOR PILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,780
PRIOR APPLICATION NUMBER: 60/201,780
PRIOR PILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,006
PRIOR APPLICATION NUMBER: 60/201,007
PRIOR PILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,007
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
                                                                                                                                                                         SOFTWARE: PatentIn Ver.
SEQ ID NO 41
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                                          Query Match
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PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,238
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,186
PRIOR APPLICATION NUMBER: 60/201,186
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PRIOR APPLICATION NUMBER: 60/220,591
PRIOR FILING DATE: 2000-07-25
                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-01-30 NUMBER OF SEQ ID NOS: 113
                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/265,160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-05-03
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PRIOR APPLICATION NUMBER: 60/201,474
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                                                                                                                                  LENGTH: 1663
TYPE: PRT
Local Similarity nes 13; Conserv
                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-09-15
APPLICATION NUMBER: 60/263,217
                                                                                                                                                                                                                                                                                       FILING DATE: 2001-01-22
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Taupier, Raymond J
Grosse, William M
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Alsobrook II, John
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Gangolli, Esha A
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Padigaru, Muralidhara
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Spytek, Kimberly A
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Zerhusen, Bryan D
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  100.0%; Score 70; DB 11; ilarity 100.0%; Pred. No. 0.0063; Conservative 0; Mismatches 0
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US-09-845-715-1
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Best Local Similarity
Marches 12; Conserva
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US-09-846-349-1
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-846-349-1
Sequence 1, Application US/09845731
Publication No. US20030004307A1
GENERAL INFORMATION:
APPLICANT: Jackowski, George
TITLB OF INVENTION: Biopolymer Marker Indicative Of Disease State Having A Molecular
TITLE OF INVENTION: 0f 1211 Daltons
FILE REFERENCE: 2132.029
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
S-09-845-715-1
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APPLICANT: Jackowski, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
TITLE OF INVENTION: OF 1348 DALTONS
FILE REFERENCE: 2132.030
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Patent No. US200
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CURRENT FILING DATE: 2001-04-30
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TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
TITLE OF INVENTION: OF 1449 DALTONS
FILE REFERENCE: 2132.034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/846,349
CURRENT FILING DATE: 2001-04-30
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11; Conserv
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US20020161184A1
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100.0%; Pred. No.
tive 0; Mismatcl
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0.0016;
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; Sequence 42, Application US/09842758
; Publication No. US20030083244A1
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i' TYPE: PRT
i ORGANISM: Homo sapiens
US-09-845-731-1
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PRIOR FILLING DATE: 2000-04-28
PRIOR PELICATION NUMBER: 60/201,006
PRIOR FILLING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,007
PRIOR FILLING DATE: 2000-05-01
PRIOR PELICATION NUMBER: 60/201,236
PRIOR FILLING DATE: 2000-05-01
PRIOR FILLING DATE: 2000-05-01
PRIOR PELICATION NUMBER: 60/201,238
PRIOR PELICATION NUMBER: 60/201,238
PRIOR FILLING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,508
PRIOR FILING DATE: 2000-05-03
PRIOR PPLICATION NUMBER: 60/220,591
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/232,678
PRIOR APPLICATION NUMBER: 60/263,217
PRIOR APPLICATION NUMBER: 60/263,217
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Best Local Similarity
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PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 60/200,613
PRIOR FILING DATE: 2000-04-28
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CURRENT APPLICATION NUMBER: US/09/842,758
CURRENT FILING DATE: 2001-04-25
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APPLICANT: Alsobrook II, John P
TITLE OF INVENTION: NO. US200300
                                                                                                                                                        PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/
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MacDougall, John R
Taupier, Raymond J
Grosse, William M
Edward, Szekeres S
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Burgess, Catherine E
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nilarity 100.0%;
Conservative
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                                                                                                                                                        60/201,474
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Pred. No.
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RESULT 11
US-10-183-116-47
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Best Local Similarity
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US-10-183-116-45
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CURRENT FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR APPLICATION NUMBER: US 60/204,707
PRIOR APPLICATION NUMBER: US 60/205,493
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR FILING DATE: 2001-05-04
                                                                                                                                                                                                             Sequence 47, Application US/10183116 Publication No. US20030092035A1 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 321
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NUMBER OF SEQ ID NOS: 113
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 42
APPLICANT: SIMON, .... APPLICANT: Han, Sang-kyou APPLICANT: Han, Sang-kyou TITLE OF INVENTION: PAIN SIGNALING MOLECULES FILE REFERENCE: CALTE.4C1CP1
CURRENT APPLICATION NUMBER: US/10/183,116
CURRENT APPLICATION NUMBER: 2002-06-26
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Publication No.
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Best Local Similarity
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                                                                                                                                                                  APPLICANT: Anderson, David J. APPLICANT: Dong, Xinzhong
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APPLICANT: Han, Sang-kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE.4C1CP1
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TYPE: PRT
ORGANISM: Sus scrofa
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                                                                                                                      Dong, Xinzhong
Zylka, Mark
Simon, Melvin
                                                                                                                                                                                                                                                                                                                                                                                              HRIHWESASLL 13
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No. US20030092035A1
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76.9%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 15; Length 321;
1.2e+02;
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                     APPLICANT:
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FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12347
TYPE: DET
                                                                                                                                                       RESULT 13
US-10-074-475-209
                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Streptomyces avermitilis US-10-156-761-12347
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US-10-156-761-12347
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Sequence 209, Application US/10074475
Publication No. US20030092898A1
GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Hu, Ping
APPLICANT: Recipon, Herve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 47
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Best Local :
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APPLICANT:
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PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 109
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PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR FILING DATE: 2001-04-19
PRIOR FILING DATE: 2001-04-19
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PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 322
TYPE: PRT
ORGANISM: Mus musculus
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Local Similarity 54.5%;
nes 6; Conservative
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HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
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54.5%;
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Karra, Kalpana

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; SEQ ID NO 209
; LENGTH: 55
; TYPE: PRT
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-074-475-209
RESULT 15
US-10-205-219-121
; Sequence 121, Application US/10205219
; Publication No. US20030138803A1
; GENERAL INFORMATION:
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Best Local Similarity
Watches 6; Conserve
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; TYPE: PRT
; ORGANISM: Mus musculus
US-10-183-116-79
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CURRENT FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR FILING DATE: 2000-08-01
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CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 60/268,292
PRIOR FILING DATE: 2001-02-13
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PRIOR FILING DATE: 2001-05-04
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PRIOR APPLICATION NUMBER: US 60/202,027
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SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2000-05-04
APPLICATION NUMBER: US 09/704,707
FILING DATE: 2000-01-03
APPLICATION NUMBER: US 60/285,493
FILING DATE: 2001-04-19
                                                                                                                        250 HRLKWQSLKLL 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F: Han, Sang-kyou
INVENTION: BAIN SIGNALING MOLECULES
ERENCE: CALTE 4C1CP1
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Liu, Chenghua
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Zylka, Mark
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                                                                                                                                                                                          Conservative
                                                                                                                                                                                                         54.3%;
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                                                                                                                                                                                                           Score 38; DB 15; Length 268; Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Vernet, Corine A
APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richard A
APPLICANT: Herrman, John L
APPLICANT: Majumder, Kumud
APPLICANT: Mishra, Vishnu
APPLICANT: Mezes, Peter S
APPLICANT: Mezes, Peter S
                                                                Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. SEQ ID NO 68
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Patent No. US20020155115A1
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                                                                                                                                                                                                                                    APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115A1el Proteins and Nuclec Acids Encoding
FILE REFERENCE: 15966-697 CIP
CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
NUMBER OF SEQ ID NOS: 114
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CURRENT FILING DATE: 2002-07-24
                                                                                                                                                       LENGTH: 2012
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: WL-A-018200
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pinnock, Robert
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1702 VTHTVHYQSVS 1712
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                                                                                                                                                                                          2012
                                 1 ITHRIHWESAS 11
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                                                                    Conservative
                                                                                 45.5%;
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75.0%;
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Pred. No.
                                                                                 Score 38; DB 10;
Pred. No. 9.8e+02;
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                                                                                                   Length 2012;
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RESULT 17
US-09-800-198-57
; Sequence 57, Application US/09800198
; Publication No. US20030087816A1
; GENERAL INFORMATION:

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; ORGANISM: Homo sapiens
US-09-800-198-57
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SEQ ID NO 57
LENGTH: 2012
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                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26
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APPLICANT: Rastelli, Luca
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-697
CURRENT APPLICATION NUMBER: US/09/800,198
CURRENT FILING DATE: 2001-03-05
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PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 98
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nes 5; Conserv
                                                                                                                              APPLICATION NUMBER: PCT/US01/00669
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                                                                                FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: GB 24263.6 FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 09/632,366
                                APPLICATION NUMBER: PCT/US01/00663
                                                  APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00667
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                FILING DATE:
APPLICATION NUMBER: PCT/US01/00662
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Herrmann, John L
Majumder, Kumud
Mishra, Vishna
Mezes, Peter S
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Chen, Wensheng
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l, David K.
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9.8e+02;
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APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REPERENCE: Acomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-03

PRIOR APPLICATION NUMBER: US 60/23,366

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00669

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APPLICANT: Penn, Sharron
APPLICANT: Rank, David |
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-6-30
PRIOR APPLICATION NUMBER: US 09/774,203
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N: EXPRESSED IN HBL100, SIGNAL = 0.99

N: EXPRESSED IN HEART, SIGNAL = 0.92

N: EXPRESSED IN LUNG, SIGNAL = 1.9

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.4

N: EXPRESSED IN BRAIN, SIGNAL = 1.2

N: EXPRESSED IN BRAIN, SIGNAL = 1.1

N: EXPRESSED IN BAJULT LIVER, SIGNAL = 1.1

N: EXPRESSED IN BH541030.1, EVALUE 7.00e-17

N: SMISSPROT HIT: P14336, EVALUE 3.60e+00
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CURRENT FILING DATE: 2001-05-23
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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                                                               APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
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APPLICATION NUMBER: US 09/632,366
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APPLICATION NUMBER: US 09/608,408
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APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                        FILING DATE: 2001-01-30
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US20020048763A1
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Hanzel, David K.
Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
: 2001-01-30
NUMBER: PCT/US01/00665
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EST_HUMAN HIT: BE877915.1, EVALUE 1.10e-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.9%;
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SED IN LUNG,
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IN PLACENTA, SIGNAL = 1
IN ADULT LIVER, SIGNAL = 0.9
IN FETAL LIVER, SIGNAL = 0.93
IN BRAIN, SIGNAL = 0.93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB Pred. No. 61; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL = 1.1
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BD
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RESULT 21
US-09-864-761-46114
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                                                             CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERNAL BERN
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 49117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
                                           PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT:
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 THRIPWSLAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel, David F
Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank, David R.
Hanzel, David K.
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EXPRESSED IN FETAL I
EXPRESSED IN BOT474,
EXPRESSED IN BONE MEXPRESSED IN HBL100
   2000-09-27
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                                   US 60/236,359
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Pred. No.
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ADULT LIVER, SIGNAL = 1.7
BRAIN, SIGNAL = 2
HEART, SIGNAL = 1.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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FILING DATE:

APPLICATION NUMBER: PCT/US01/00667

2001-01-3

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APPLICANT: Graff, Jonathon M.
APPLICANT: Mienster, Matthew
TITLE OF INVENTION: METHADS TO IDENTIFY SIGNAL SEQUENCES
FILE REFERENCE: A34943 090495.0243
CURRENT APPLICATION NUMBER: US/10/002,631C
CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 60/300,309
PRIOR FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 324
SOFFWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 135
LENGTH: 151
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                               US-10-002-631C-135
Sequence 135, Application US/10002631C
Publication No. US20030157486A1
GENERAL INFORMATION:
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Best Local S
Matches 7
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SEQ ID NO 46114
LENGTH: 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: MAP TO ACOO6548.20
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
OTHER INFORMATION: SWISSPROT HIT: Q09312, EVALUE 6.00e-37
FEATURE:
NAME/KEY: UNSURE
LOCATION: (136)...(136)
                                                                    ORGANISM: Mus musculus
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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APPLICATION NUMBER: PCT/US01/00661
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Pred. No. 1.1e
0; Mismatches
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1.1e+02;
hes 3;
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RESULT 24
US-10-139-814-12
; Sequence 12, Application US/10139814
; Publication US20030134790A1
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/089,818B
FILING DATE: June 3, 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, STEVEN R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 32,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            Matches
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APPLICANT: Langenfeld, John
TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-2 IN THE TREATMENT AND DIAGNOSIS OF
TITLE OF INVENTION: CANCER
FILE REFERENCE: 273/136 Michael J. Wise
CURRENT APPLICATION NUMBER: US/10/139,814
CURRENT FILING DATE: 2002-05-02
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APPLICANT: Follettie, Maximillian
APPLICANT: DeRobertis, Edward M.
TITLE OF INVENTION: Mammalian Cerberus-Like Protein
TITLE OF INVENTION: Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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TOPOLOGY: linear
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87 CambridgePark Drive
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NO: 8:
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85.7%;
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Pred. No. 1.3e
0; Mismatches
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Pred. No. 2.1e+02;
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US-10-044-716-12
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; ORGANISM: homo sapiens
US-10-286-152A-52
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                                                                                        Sequence 12, Application US/10044716
Publication No. US20020159986A1
GENERAL INFORMATION:
APPLICANT: LANGENFELD, John
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LENGTH: 267
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Best Local Similarity
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NAME/KEY: misc_feature
LOCATION: (361)..(741)
OTHER_INFORMATION: DAN d
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            TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-2 IN THE TREATMENT AND DIAGNOSIS FILE REFERENCE: 270/070US
CURRENT APPLICATION NUMBER: US/10/044,716
CURRENT FILING DATE: 2002-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Alcon Research, APPLICANT: Clark, Abbot F
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PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
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PRIOR APPLICATION NUMBER: US60/261,252
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LOCATION: (484)..(723)
OTHER_INFORMATION: Cysteine knot region
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LOCATION: (490)..(723)
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TYPE: PRT
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Local Similarity 50.0%;
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Pred. No. 2.1e+02;
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Pred. No.
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TYPE: PRT
ORGANISM: Mus musculus
US-09-887-552A-2
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US-09-089-818B-2
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                 Sequence 2, Application US/09089818B
Patent No. US20020164682A1
GENERAL INFORMATION:
APPLICANT: Follettie, Maximillian
APPLICANT: DeRobertis, Edward M.
TITLE OF INVENTION: Mammalian Cerberus-Like Protein
TITLE OF INVENTION: Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/282,668
PRIOR FILING DATE: 2001-04-09
NUMBER OF SEQ ID NOS: 4
SOPTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 2
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NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
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                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches 4; Conserv
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PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: US 60/266,046
PRIOR FILING DATE: 2001-02-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Brennan, Thomas J.
APPLICANT: Leviten, Michael W.
TITLE OF INVENTION: TRANSCENIC MICE CONTAINING CERBERUS GENE
TITLE OF INVENTION: DISRUPTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (361)...(741)
OTHER INFORMATION: DAN domain
NAME/KEY: misc feature
LOCATION: (484)...(723)
OTHER INFORMATION: Cysteine knot region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: C-terminal cysteine knot-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (490)..(723)
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NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                           154 SHEVHWET 161
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                                                                                                                                                                                                                                                                                                                  52.9%;
Compositions
12
                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                  Score 37; I
Pred. No. 2.
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Pred. No.
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CORRESPONDENCE ADDRESS:

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; OTHER INFORMATION: Xaa
US-10-106-698-4945
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/153,280
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4945, Application US/10106698 Publication No. US20030109690A1
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                                  OTHER INFORMATION: XAA 6
NAME/KEY: MISC FEATURE
LOCATION: (201)
OTHER INFORMATION: XAA 6
NAME/KEY: MISC FEATURE
LOCATION: (242)
                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 3.0

SEQ ID NO 4945

LENGTH: 292

TYPE: PRT
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                                                                                                                                                                  FEATURE:
NAME/KEY: MISC FEATURE
                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/089,818B FILLING DATE: June 3, 1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, STEVEN R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 8/ Cambridge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 272 amino TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
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87 CambridgePark Drive
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(617) 876-5851
TD NO: 2:
               equals any of the naturally occurring L-amino acids
                                                                                                                                      equals any of the naturally occurring L-amino acids
                                                                           equals any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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Pred. No. 2.2e+02;
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                                                                             L-amino acids
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US-10-139-262-2
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Sequence 2, Application US/10139262 Publication No. US20020128459A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 5; Conserv
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SEQ ID NO 93
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001/09/26
PRIOR FILING DATE: 2001/09/26
PRIOR FILING DATE: 2001/09/26
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/325,102 PRIOR FILING DATE: 2001-09-26
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PRIOR FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                    Similarity 5; Conserv
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Shubhangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
                                                                                                                               LTORVHWAEA 52
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Karen GLATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gordon B. MILLS
Robert C. BAST, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ami SEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Karen LU
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50.0%;
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Pred. No. 2.3e+02;
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Pred. No. 2
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                                                                                                                                                                                                        Mismatches
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RESULT 33
US-09-764-891-4103
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CURRENT APPLICATION NUMBER: US/10/255,969
CURRENT FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: US/09/380,287
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: JP 1997-62259
PRIOR FILING DATE: 1997-02-28
PRIOR FILING DATE: 1997-02-28
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 42
NUMBER OF SEQ ID NOS: 42
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; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-139-262-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: US/09/380,287A
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: JP 1997-62259
PRIOR FILING DATE: 1997-02-28
PRIOR APPLICATION NUMBER: JP 1998-62263
PRIOR FILING DATE: 1998-02-25
                                                                                Sequence 4103, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 52.9%;
Best Local Similarity 41.7%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                       APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NAKAMURA, YUSUKE
APPLICANT: TANAKA, TOSHIHIRO
APPLICANT: TSUKADA, SHUICHI
CURRENT APPLICATION NUMBER: US/09/764,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1
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CURRENT FILING DATE: 2002-05-07
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TITLE OF INVENTION: PHYSIOLOGICALLY ACTIVE PROTEIN ORIGINATING IN MAMMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: PHYSIOLOGICALLY ACTIVE PROTEIN ORIGINATING IN MAMMALS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 385
TYPE: PRT
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Local Similarity 41.7%;
1es 5; Conservation
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                                                                                                                                                                                                                                                                                       1 ITHRIHWESASL 12
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TSUKADA, SHUICHI
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Pred. No. 3e+02;
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Pred. No. 3e+02;
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Query Match
Best Local Similarity
Matches 6; Conserv:
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US-10-103-313-418
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                                                                                                                  US-10-103-313-541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 418
LENGTH: 390
                                                                                                                                                            NUMBER OF SEQ ID NOS: 653
Prior Application removed -
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 541
LENGTH: 390
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ07C1
                                                                                                                                                                                                                                                                                                                             Sequence 541, Appublication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 418, Application US/10103313
Publication No. US20030082758A1
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                                                                                    Query Match
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                                                                                                                                                                                                                                                                APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ07C1
                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
                                                                                                                                               LENGTH: 39
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                                                                                                                                ORGANISM: Homo sapiens
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                                                      Local Similarity nes 6; Conserv
333 ITHNIHYEN 341
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                          ITHRIHWES 9
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o. US20030082758A1
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Pred. No.
                                                                    Score 37; DB 15;
Pred. No. 3.1e+02;
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Pred. No. 3.1e+02
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 130 —
; OTHER INFORMATION: Xaa is Tyr or His or Gln or Asn or Lys or Asp or Glu
US-10-255-969-6
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, NAME/KEY: misc_feature
, LOCATION: 130 -
; OTHER INFORMATION: Xaa is Tyr or His or Gln or Asn or Lys or Asp or Glu
US-10-139-262-6
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Query Match
Best Local Similarity
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PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: JP 1997-622:
PRIOR FILING DATE: 1997-02-28
PRIOR APPLICATION NUMBER: JP 1998-6226
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: JP
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 42
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PRIOR TILING DATE: 199-11-16
PRIOR APPLICATION NUMBER: JP 1997-6225
PRIOR FILING DATE: 1997-02-28
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CURRENT FILING DATE: 2002-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/255,969
CURRENT FILING DATE: 2002-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: NAKAMURA, YUSUKE
APPLICANT: TANAKA, TOSHIHIRO
APPLICANT: TSUKADA, SHUICHI
                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PHYSIOLOGICALLY ACTIVE PROTEIN ORIGINATING IN MAMMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver.
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TITLE OF INVENTION: PHYSIOLOGICALLY ACTIVE PROTEIN ORIGINATING IN MAMMALS
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APPLICANT: TANAKA, TOSHIHIRO
                                                                                                                                                                LENGTH: 433
TYPE: PRT
ORGANISM: Mus musculus
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TYPE: PRT
ORGANISM: Mus musculus
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52.9%;
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Pred. No. 3.4e+02;
5; Mismatches 2
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Score 37; DB 15;
Pred. No. 3.4e+02;
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US-10-255-969-4
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US-10-139-262-4
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APPLICANT: NAKAMURA, YUSUKE
APPLICANT: TANAKA, TOSHIHIRO
APPLICANT: TSUKADA, SHUICHI
TITLE OF INVENTION: PHYSIOLOGICALLY ACTIVE PROTEIN ORIGINATING IN MAMMALS
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Publication No. US20020128459A1
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                                                       Query Match
Best Local
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PRIOR APPLICATION NUMBER: US/09/380,287
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: JP 1997-622:
PRIOR FILING DATE: 1997-02-28
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CURRENT APPLICATION NUMBER: US/10/255,969
CURRENT FILING DATE: 2002-09-27
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PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: JP 1997-62255
PRIOR FILING DATE: 1997-02-28
PRIOR APPLICATION NUMBER: JP 1998-62263
PRIOR FILING DATE: 1998-62263
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 42
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CURRENT FILING DATE: 2002-05-07
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APPLICANT: TANAKA, 7
APPLICANT: TSUKADA,
                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: TSUKADA, SHUICHI
TITLE OF INVENTION: PHYSIOLOGICALLY ACTIVE PROTEIN ORIGINATING IN MAMMALS
                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 42
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TYPE: PRT
                                                                                                                                                    TYPE: PRT
                                                                                                                                                                    ENGTH:
                                                     Local
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1 ITHRIHWESASL 12
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Similarity 41.7%;
5; Conservative
                                   Similarity 41. 5; Conservative
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Pred. No. 3.4e+02;
                                 Score 37; DB 15;
Pred. No. 3.4e+02;
5; Mismatches 2;
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GENERAL INFORMATION:

APPLICANT: Walke, D. Wade
APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Johan
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Hu, Yi
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Hu, Yi
APPLICANT: Hu, Yi
APPLICANT: WINGER: US20020115838A1el Human Proteases and Polynucleotides Encodin
FILE OF INVENTION: NOWBER: US 0/227,104
FILE REFERENCE: LEX-0237-USA
CURRENT FILING DATE: 2031-08-22
PRIOR APPLICATION NUMBER: US 60/227,104
FRIOR APPLICATION NUMBER: US 60/223,796
FRIOR FILING DATE: 2000-09-19
INVENTIALE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 451
TYPE: PRT
ORGANISM: homo sapiens
US-09-938-330-2
Search completed: August 28, 2003, 14:22:54 Job time : 58 secs
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US-09-938-330-2
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Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09938330 Patent No. US20020115838A1 GENERAL INFORMATION:
                                                                                                          434 HRFHWSRCSKL 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::| ::|| :||
410 LSHSLYWEVSSL 421
                                                                                                                                                 3 HRIHWESASLL 13
                                                                                                                                                                                                              Score 37; DB 10; Length 451; Pred. No. 3.5e+02; 0; Mismatches 5; Indels
                                                                                                                                                                                                                 0;
                                                                                                                                                                                                              Gaps
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
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Match
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283308 seqs, 96168682 residues
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        280
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A82997
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                                               Per coordinate of the coordina
gene UL9 protein -
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ALIGNMENTS

108	
	C3HU .
	<pre>complement C3 precursor [validated] - human N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit; (</pre>
	C; Species: Homo sapiens (man)
	C;Date: 28-Aug-1985
	R;de Bruijn, M.H.L.; Fey, G.H. Proc. NatlAcadSciU.S.A82,_708-712,_1985
	-A-TITTE: Human Complement Component C3: CUNA coding sequence and derived primary structue. A.Reference number: A94065; MUID:85140166; PMID:2579379
	A; Molecule type: mRNA
to have a	A. Gross references: GB.VO.VIGE. NID. G170664. DIDN. NANOSANA 1. DID. G170665
being printed,	R;Vik, D.P.; Amiguet, P.; Moffat, G.J.; Fey, M.; Amiguet-Barras, F.; Wetsel, R.A.; Tack,
ition.	Biochemistry 30, 1080-1085, 1991 A:Title: Structural Features of the human C3 gene: intron/exon organization, transcription of the human C3 gene.
	A)Reference number: A37999; MUID:91113687; PMID:1703437
	A;Contents: intron/exon structure of gene
Description	A;Molecule type: DNA
	A;Residues: 1-25 «VIX»
complement C3 - ra	A; Note: the authors translated the codon GGT for residue 6 as Leu. CCC for residue 7 as
hypothetical prote	R;Hugli, T.E.
MP3 protein - yea	J. Biol. Chem. 250, 8293-8301, 1975
prothetical prote	A: Reference number: A92187: MIID: 76069169: PMID: 1238393
ypothetical prote	A;Accession: A92187
ypothetical cytos	A; Molecule type: protein
ypochecical proce	A;Residues: 672-680,'N',682-699,'Q','701-748 <hug></hug>
ABC transporter re	J. Immunol. 140, 1577-1580, 1988
ABC transporter re	A; Title: A 34-amino acid peptide of the third component of complement mediates properdin
Sonserved hypothet	A;Reference number: A27603; MUID:88154452; PMID:3279119 A:Acression A27603
ypothetical prote	A; Molecule type: protein
ypothetical prote	A; Residues: 1409-1563 < DAO>
hypothetical prote	k;Hellman, u.; Eggertsen, u.; Engertom, A.; Sjoquist, u. Biochem. u. 230, 353-361, 1985
lown syndrome cell	A;Title: Amino acid sequence of the trypsin-generated C3d fragment from human complement
Jutamine-fructose	A; Reference number: A23435; MUID: 86025442; PMID: 3876831
onserved hypothet	A:MCCEBBLON: A23435 A:MOlecule type: protein
ypothetical prote	A; Residues: 1002-1012, E; 1014-1303 < HEL>
protein T10022.23	A; Note: sequence corresponding to residues 1072-1100 was not determined but was taken fro
pothetical prote	J. Immunol. 143, 1254-1258, 1989
onserved hypothet	A; Title: The difference between human C3F and C3S results from a single amino acid change
gene UL9 protein -	A;Reference number: A45830; MUID:89309808; PMID:2473125

```
F;1424-1457/Region: properdin binding
F;85,939/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;85,939/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;559-816,627-662,693-720,694-727,707-728,873-1513,1101-1158,1358-1489,1389-1458,1506-15
F;748-749/Cleavage site: Arg-Ser (C3 convertase) #status predicted
F;954-955/Cleavage site: Arg-Glu (complement factor I) #status predicted
F;1010-1013/Cross-link: thiolester (Cys-Gln) #status experimental
F;1303-1304/Cleavage site: Arg-Ser (complement factor I) #status predicted
F;1300-1321/Cleavage site: Arg-Ser (complement factor I) #status predicted
F;1300-1301/Cleavage site: Arg-Ser (complement factor I) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: alpha-2-macroglobulin
C;Superfamily: alpha-2-macroglobulin
C;Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein;
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-667/Product: complement C3 and C3b beta chain #status predicted <C3b>
F;23-667,672-1663/Product: complement C3 #status predicted <C3B>
F;23-667,749-1663/Product: C3b #status predicted <C3B>
F;672-1663/Product: C3b anaphylatoxin #status predicted <C3T>
F;672-1663/Product: C3a anaphylatoxin #status predicted <C3BA>
F;749-1663/Product: C3b fragment #status predicted <C3BA>
F;946-1303/Product: C3ds fragment #status predicted <C3G>
F;955-1001/Product: C3d fragment #status predicted <C3G>
F;955-1001/Product: C3d fragment #status predicted <C3G>
F;1002-1303/Product: C3d fragment #status predicted <C3G>
F;
                                                                                                                                                                                                                                                                                                                                                                                                            complement C3 - rabbit (fragment)
N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) (
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 15-Dec-1988 #sequence_revision 07-Oct-1994 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Contents: annotation; disulfide bonds
C;Comment: The sequence shown is the C3 fast (C3F) allele, which is found mainly in Cauc
C;Comment: Complement C3 contains two chains, formed by removal of four residues and lin
alternative complement pathways, releases the C3a anaphylatoxin from the amino end of t
rnative-complement-pathway C3/C5 convertase.
C;Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.
C;Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign pa
e classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by pro
C;Comment: The major site of synthesis of this plasma protein is the liver.
                                                                                                                                                                                                              R;Kusano, M.; Choi, N.H.; Tomita, M.; Yamamoto, K.; Migita, S.; Sekiya, T.; Nishimura, (Immunol. Invest. 15, 365-378, 1986
A;Title: Nucleotide sequence of cDNA and derived amino acid sequence of rabbit complements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Dolmer, K.; Sottrup-Jensen, L.
FEBS Lett. 315, 85-90, 1993
A;Title: Disulfide bridges in human complement component C3b.
A;Reference number: S27041; MUID:93106233; PMID:8416818
                                                                                                       A;Reference number: A27602; MUID:87006907; A;Accession: A27602
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A;Cross-references: GDB:119044;
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A; Residues: 1212-1223 < PO2>
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A; Accession: B45830
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A; Residues: 1212-1215, 'N', 1217-1223
                                                   A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                               C; Accession: A27602
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Best Local S
Matches 13
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1-726 <KUS>
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Pred. No. 0.00065;
; Mismatches 0;
                                                                                                                                                                PMID:3019881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subunit;
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A;Cross-references: GB:M32434; NID:gl64862; PIDN:AAA31190.1; PID:gl64863 C;Comment: Complement C3 contains two chains, formed by removal of four residues and lin alternative complement pathways, releases the C3a anaphylatoxin from the amino end of tirrative-complement-pathway C3/C5 convertage.

C;Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation. C;Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign paed classical-complement-pathway C3/C5 convertage. The activity of C3b is regulated by procycomment: The major site of synthesis of this plasma protein is the liver.

C;Superfamily: alpha-2-macroglobulin

C;Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein;
                                                                                A;Residues: 1-516 <BOR>
A;Residues: 1-516 <BOR>
A;Cross-references: EMBL:275057; NID:g1420374; PID:e252038; PID:g1420375; MIPS:YOR149c A;Experimental source: strain S288C
A;Experimental source: strain S288C
R;Irie, K.; Araki, H.; Oshima, Y.
Mol. Gen. Genet. 225, 257-265, 1991
                                                                                                                                                                                                                                                                                                              C;Accession: S67037; S13750
R;Bordonne, R.; Camasses, A.; Madania, A.; Martin, submitted to the Protein Sequence Database, July 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Complete genome sec
A;Reference number: A82950;
A;Accession: A82997
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Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein PA5194 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: A82997
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A;Title: Mutations in a Saccharomyces cerevisiae host showing A;Reference number: $13750; MUID:91172125; PMID:2005867 A;Accession: $13750
                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-516 <B
                                                                                                                                                                                                                                                              A;Reference number: S67032
A;Accession: S67037
                                                                                                                                                                                                                                                                                                                                                                                                  SMP3 protein - yeast (Saccharomyces cerevisiae)
N,Alternate names: protein O3527; protein YOR149c
C;Species: Saccharomyces cerevisiae
C;Species: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 21-Jul-2000
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 21-Jul-2000
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A; Residues: 1-267 <STO>
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Best Local
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50; MUID:20437337; PMID:10984043
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58.3%;
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Pred. No. 1.
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Pred. No. 1.4;
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K.; Lim,
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A;Molecule type: DNA
A;Residues: 1-121,'IK',124-162,'G',164-168,'R',170-278,'L',280-516
A;Cross-references: EMBL:X58121; NID:g4497; PIDN:CAA41123.1; PID:g4

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A;Cross-references: GB:AE004080; GB:AE003849; NID:g9107971; PIDN:AAP85520.1; GSPDB:GN001 A;Experimental source: strain 9a5c R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Asriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Catraro, D.M.; Carrer, F. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Faigr. J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.S.; Laigr.
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A;Note: for a complete list of authors see reference number A59328 bei
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A; Residues: 1-211 <STO>
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Nature 406, 959-964, 2000
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A;Cross-references: SGD:S0005675; MIPS:YOR149c
                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-401 <SIM>
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                                                                                                                                                                                                                                                             A;Accession: E82521
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Best Local
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Similarity 63.6%;
7; Conservation
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#status predicted <TM5>
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Pred. No. 5.6;
4; Mismatches
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Pred. No.
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K.; Lim,
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A;Gene: BMEI0303 A;Map position: C;Superfamily: R:

;Map position: I ;Superfamily: Rickettsia

prowazekii hypothetical protein RP073

Query Match

Local Similarity

57.1%; 58.3%;

Score Pred.

No. DB 14;

2

A; Experimental source: strain

Genetics:

A;Molecule type: DNA A;Residues: 1-229 <KUR> A;Cross_references: GB;AE008917; PIDN:AAL51484.1;

PID:g17982196;

GSPDB:GN00190

Status: preliminary

R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesso Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens;Reference number: AD3252; PMID:11756688 ;Recession: AI3289

hypothetical cytosolic protein BMEI0303 (imported) - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002

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A;Accession: B86713
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A;Contents: annotation
C;Genetics:
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C;Superfamily: Mycobacterium tuberculosis probable
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A;Molecule type: DNA
A;Residues: 1-615 <STO>
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                                                                                                                                                                    Matches
                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GB:AE005176; PID:g12723617; PIDN:AAK04804.1; GSPDB:GN00146
Experimental source: strain IL1403
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                                                                                                                                                                                                  Local Similarity
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                                                                             2 THRIHWESA 10
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THRLHWLSS
                                                                                                                                                                    Conservative
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517
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45.5%;
                                                                                                                                                                                                      Score 41;
Pred. No.
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Pred. No. 11;
                                                                                                                                                                    Mismatches
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27;
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
C;Accession: C69611
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
'Atthes 6; Conserva
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    R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Az C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret,
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A; Residues: 1-259 < BRA>
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A; Accession: T29569
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R;Bradshaw, H.; Stellyes, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein C44C1.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
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A, Accession: T50894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, November 1999
A;Description: Determination of Nucleotide Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Nagashima,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: CESP: C44C1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C44C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
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;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                192 RLHWDGESLL
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ily: Caenorhabditis elegans hypothetical protein C44Cl.1
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                                                                                                        required for expression of cytochrome llus subtilis
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                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: U41030; PIDN: AAA82366.1; CESP: C44C1.1
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                                                                                                                                                                                                                                                                                                                                     55.7%;
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75.0%;
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Pred. No. 16;
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Pred. No.
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                                                                                                                            (ATP-)
                                                                                     02-Feb-2001
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    Azevedo, V
7.; Carter,
cet, C.; Fei
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                                                                                                                              subtilis
    Berter
M.; Cho
ri, E.
                                                                RESULT 13
AC1414
ABC transporter required for expression of cytochrome BD homolog cydC [imported] C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
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A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler. iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Accession: C69611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma. A;Authors: Kreft, U.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Tittle: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1790
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                                                                                                                                                                                                                                     C; Superfamily: Mycobacterium tuberculosis probable
                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AL592022; PIDN:CAC98090.1; PID:g16415399; GSPDB:GN00178
A;Experimental source: strain Clip11262
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A;Molecule type: DNA
A;Residues: 1-574 <GLA>
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A;Residues: 1-567 <KUN>
A;Cross-references: GB:Z99123; GB:AL009126; NID:g2636240; PIDN:CAB15900.1; PID:e1186373;
A;Experimental source: strain 168
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.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; F
D.; Jones, L.M.; Karst, U.
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                                                                                                                                                Query Match
Best Local
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Best Local
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                                                                                                                    Matches
   527
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                                                                                                                 Similarity 5; Conserv
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                                                          THRIHW 7
                                                                                                                    Conservative
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83.3%;
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83.3%;
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                                                                                                                    1; Mismatches
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Fsihi, H.
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C;Accessio
R;Glaser,
                                                                                                            hypothetical protein Rv1085c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                      Rajandream, M.A.; Rogers, J.; Rutter, Nature 393, 537-544, 1998
                                                         R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harri, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin,
                                                                                                    C; Accession: C70895
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A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1414
                                                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-228 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL43727.1;
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyav; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:NC_003210;
A;Experimental source: strain EGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: The Genome of the Natural Genetic A; Reference number: AB2577; MUID:21608550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Authors: Yoo, H.; Tao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-574 <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: Rickettsia
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Superfamily: Mycobacterium tuberculosis probable
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; Jones, L.M.; Karst, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            position: circular chromosome
prfamily: Rickettsia prowazekii hypothetical
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  Sulston, J.E.; Taylor, K.; Whitehead,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y.; Biddle, P.; Jung, M.; Krespan,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB
Pred. No. 56;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                         Score 38;
Pred. No.
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                                    S.; Seeger, K.; Skelton, S.; Squares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Engineer Agrobacterium tumefaciens PMID:11743193
                                                                                                                                                                                                                                                                                                                                                            31;
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D.; Kutyavin, T.; Levy, R.; Li, M.;
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  S.; Barrell, B.G
                                                                           C.; Harris,
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                                                       Holroyd,
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Fsihi, H.
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Query Match
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A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70895
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-242 <COL>
A;Cross-references: GB:AL021897; GB:AL123456; NID:g3256022; PIDN:CAA17201.1; PID:g289672
A;Experimental source: strain H37Rv
   A;Cross-references: SGD:S0001109
A;Map position: 8R
C;Superfamily: Saccharomyces hyp
                                                                                       A;Molecule type: DNA
A;Residues: 1-280 <LAT>
A;Cross-references: EMBL:U00061; NID:g487943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
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A;Map position: circular of
C;Superfamily: Rickettsia
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A; Residues: 1-266 < KUR>
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                                                           A; Gene: MIPS: YHR067w
                                                                                                                                                    A; Accession: S46699
                                                                                                                                                                    A; Reference number: S46696
                                                                                                                                                                                        A; Description: The sequence
                                                                                                                                                                                          submitted to the EMBL Data Library, May 1994
A;Description: The sequence of S. cerevisiae
                                                                                                                                                                                                                                                                                                                           hypothetical protein YHR067w -
                                                                                                                                                                                                                                                                                                                                                   S46699
                                                                                                                                                                                                                                                                                                                                                                    RESULT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 30-Sep-2001 #sequence_revision C;Accession: D97688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein AGR C 4981 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: Rv1085c
C;Superfamily: hemolysin III
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                                                                                                                                                                                                                                                                 ;Alternate names: hypothetical protein;Species: Saccharomyces cerevisiae;Date: 28-Oct-1994 #sequence_revision
Superfamily: Saccharomyces hypothetical protein YHR067w;
                                                                                 Genetics:
                                                                                                                                                                                                                                    ;Latreille,
                                                                                                                                                                                                                                                   Accession:
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l protein H8025.4
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Pred. No.
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Pred. No.
                                                                                                                                                                                            cerevisiae
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33;
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                                                                                             PID:g487947; GSPDB:GN00008; MIPS:YHR067w
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Markelz,
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rkelz, B.;
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54.3%;

Score 38;

DB

2

Length 280;

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Down syndrome cell adhesion protein 1 - human (fragment)
N;Alternate names: Down syndrome cell adhesion molecule
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: T08851
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A;Reference number: Z19481
A;Accession: T21876
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 RESULT 20
AB0500
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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                                                                                                                                                                                                                                                                             A; Note: derived from alternately-spliced mRNA
                                                                                                                                                                                                                                                                                                                                    A; MOLECULE .... CYAM's A; Residues: 1-1896 CYAM's A; Residues: 1-1896 CYAM's A; Cross-references: EMBL: AF023449; NID: g3169765; PID: g3169766 A; Cross-references: EMBL: AF023449; NID: g3169765; PID: g3169766
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                                                                                                                                                                                                                                                                                                                   A;Gene: DSCAM
                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: T08851
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                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: mRNA
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5; Conservative
                                                                                                                                                 5
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45.5%;
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1; Mismatches
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A;Cross-references: GB:AE004009; GB:AE003849; NID:g9106980; PIDN:AAF84700.1; GSPDB:GN001
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: C82625
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
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S16511
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 03-Jun-2002
C;Accession: AB0500
R; Phomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, R,Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Bruinenberg, P.G.; Evers, M.; Waterham, H.R.; Kuipers, Biochim. Biophys. Acta 1008, 157-167, 1989
A;Title: Cloning and sequencing of the peroxisomal amine A;Reference number: S04963; MUID:89287321; PMID:2500147 A;Accession: S16511
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A; Molecule type: DNA
A; Residues: 1-227 <S
                                                                                                                                                                                                                                                                   conserved hypothetical protein XF1894 [imported] - Xylella fastidiosa (strain C;Species: Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                      C82625
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C;Species: Pichia angusta
C;Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 20-Apr-2000
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C;Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
C;Keywords: aminotransferase; intramolecular oxidoreductase; isomerase
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8; Conserv
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Pred.
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Pred. No. 1
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protein T10022.23 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C66317
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.;
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; De
ansen, N.F.; Hughee, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; M
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.;
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Abriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigrando, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, H. A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A.S.; M.S.; Vettore, A.L.; Z.S.; M.S.; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein T30A10.110 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A; Residues: 1-249 <BEV>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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Pred. No.
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Pred. No. 46;
                                                                                                                                                                                                                                                                                                          C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                    ; Khaykin, E.
; Maiti, R.;
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                                                                                                          H.; Tallon,
                                                                                                                                                                                               E., Kim,
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      Query Match
Best Local Similarity
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A;Accession: C86317
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-280 <STO>
                                                                      A; Map position: 2
A; Introns: 120/1; 183/3
C; Superfamily: Caenorha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Connor, R.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Scuares Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: T10022.23
                                                                                                                                                                                  A;Cross-references: EMBL:Z81124; PIDN:CAB03373.1; GSPDB:GN00020; CESP:T21B4.5 A;Experimental source: clone T21B4
                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-341 <WIL>
                                                                                                                                                                                                                                                                                           A; Reference number: A; Accession: T25052
                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, October 1996 A;Reference number: Z19974
                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-314 <COL>
A;Cross-references: GB:Z98209; GB:AL123456; NID:g3261838; PIDN:CAB10903.1; PID:g2292961
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \lambda_{\rm f} Status: preliminary; nucleic acid sequence not shown; translation \lambda_{\rm f} Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                A; Experimental source: clone
                                                                                                                                                                                                                                                                    A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                             R;Smye, R.
                                                                                                                                                                                                                                                                                                                                                                                C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: miaA
C;Superfamily: delta(2)-isopentenylpyrophosphate transferase
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C;Species: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein T21B4.5 - Caenorhabditis elegans
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Matches
                                                                                                                                         Gene: CESP:T21B4.5
                                                                                                                                                                Genetics:
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les 5; Conserv
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                                                                    Caenorhabditis hypothetical protein C49G7.2
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    52.9%;
66.7%;
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Pred. No.
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Pred. No. 6
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DB
72;
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65;
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Score Pred.

37; No.

2

Length

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R;Maekawa, T.; Ohtsubo, E.
Jpn. J. Genet. 69, 269-285, 1994
A;Title: Identification of the region that
A;Reference number: I56963; MUID:94361836;
A;Accession: I76577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-421 <STO>
A;Cross-references: GB:AL450380; NID:g13093060; PIDN:CAC31433.1; GSPDB:GN00147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.;
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; R.; Davies, R.M.; Devlin, K.; Duthoy, S.; leam, M.A.; Rutherford, K.M.
   RESULT
WMBEU9
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A;Title: Sequence of a transposon identified as Tn1000 (gamma delta).
A;Reference number: I60218; MUID:95337425; PMID:7612932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein tnpX - Escherichia coli transposon Tn1000
C;Species: Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein ML1052 [imported] -
C;Species: Mycobacterium leprae
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A;Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: I60218;
A;Accession: I60218
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                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-698 <R
                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X60200; NID:g295867; PIDN:CAA42758.1; PID:g43087
                                                                                                                                                                                                                                                                                                                                                                                                            , Molecule type: DNA
                                                                                                                                             Query Match
Best Local S
Matches 6
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                                                                         267 RLHWDWAQLL
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                                                                                                                                                            Similarity
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                                                                                                          RIHWESASLL
                                                                                                                                             Conservative
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                                                                                                                                                                                                               GB:D16449; NID:g303565; PIDN:BAA03916.1; PID:g303568
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Pred. No.
                                                                                                                                         Score 37; DB 2;
pred. No. 1.6e+02,
2; Mismatches ;
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Feltwell, T.;
                                                                                                                                                                                                                                                                                                     determines the PMID:8080658
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90;
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                                                                                                                                                                                                                                                                                                                        specificity of binding
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Holroyd,
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T18946
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A; Residues: 1-851 < MCG>
                                                                                                                         A; Map position: (A; Introns: 15/3;
                                                                                                                                                            A;Gene: CESP:C05C10.6
                                                                                                                                                                                                                                                                                     A;Reference number:
A;Accession: T24252
                                                                                                                                                                                                                                                                                                                                          R;Wilkinson,
                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type:
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A;Residues: 1-851 <M
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Best Local
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HRIHWE--SASLL 13
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A;Cross-references: GB.M19120; NID:g330226; PIDN:AAA45822.1; PID:g330234 R;MCGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; J. Gen. Virol. 69, 1531-1574, 1988 A;Title: The complete DNA sequence of the long unique region in the genom A;Reference number: A30083; MUID:88274327; PMID:2839594 A;Accession: I28133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;McGeoch, D.J.; Dalrymple, M.A.; DOLEN, A.; PICHED, C., CLAZ, J. VIROL. 62, 444-453, 1988

A;Title: Structures of herpes simplex virus type 1 genes required for replication of virua; Title: Structures of herpes simplex virus type 1 genes required for replication of virua; A;Reference number: A93040; MUID:88091053; PMID:2828807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable phospholipase activating protein C05C10.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 07-Dec-1999 C;Accession: T18946; T24252
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C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jun-2000
C;Accession: B29890; I28133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: required for replication of C;Superfamily: varicella-zoster virus gene C;Keywords: DNA binding; DNA biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene UL9 protein - human herpesvirus 1 (strain 17)
C;Species: human herpesvirus 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:Z48178; PIDN:CAA88206.1; GSPDB:GN00020; CESP:C05C10.6
A;Experimental source: clone C05C10
                                                                                                                                                                                                                              A; Experimental source: clone
                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, October 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library,
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                                                                                                                                                                                                                              Cross-references: EMBL: Z66515; Experimental source: clone R53
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                                                                                                                120/1; 155/3; 407/3; 513/1; 549/1; 593/3;
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  Conservative
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61.5%;
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Pred. No. 1.9e
3; Mismatches
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                             Score 37; DB 2;
Pred. No. 2e+02;
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Mismatches
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e 51 protein
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1.9e+02;
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                                                     DB 2;
  1:
                                                        Length 858;
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  Indels
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Gaps
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estradiol-stimulated protein ESP1 - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 25-Feb-1994 #sequence_revision 01-Sep-1995 C;Accession: S29392 C;Accession: S29392 Normann, M.; Pongs, O.
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A; Residues: 1-147 <STO>
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A;Experimental source: strain IL1403
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A;Accession: G86466
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Cross-references: GB:AE005172; NID:g5091620; PIDN:AAD39608.1; GSPDB:GN00141
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Pred. No. 43;
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                                                          #text_change 07-May-1999
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ewar, K.;
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A;Molecule type: DNA
A;Residues: 1-82,'G',83-100,102-261 <RES>
A;Cross-references: GB:L36655; NID:g556293;
                                                                                                                                                                          R;Fraser, P.; Cummings, P.; Curtis, P.
Mol. Cell. Biol. 9, 3308-3313, 1989
A;Title: The mouse carbonic anhydrase I gene contains two tissue-specific promoters.
A;Reference number: I49573, MUID:90014784; PMID:2571923
A;Accession: I49573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carbonate dehydratase (EC 4.2.1.1) I - mouse (;Species: Mus musculus (house mouse) (;Species: Mus musculus (house mouse) C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 22-Jun-1999 C;Date: 20-May-1988 #sequence_revision 21-May-1988 #text_change 22-Jun-1999 C;Date: 20-May-1988 #sequence_revision 21-May-1988 #text_change 22-Jun-1999 C;Date: 20-May-1988 #sequence_revision 21-May-1988 #se
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Fraser, P.J.; Curtis, P.J.
J. Mol. Evol. 23, 294-299, 1986
A;Title: Molecular evolution of the carbonic anhydrase genes:
A;Reference number: A26344; MUID:87169766; PMID:3104601
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C;Superfamily: 1
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A;Experimental source: strain H37Rv
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                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-261 < FRA>
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A; Residues: 1-164 < NAL>
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                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
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Accession: C70542
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Species: Mycobacterium tuberculosis
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A; Accession preliminary
A; Status; preliminary
A; Molecule type: DNA
A; Residues: 1-291 < KUR>
A; Cross-references: GB:BA000019; PIDN:BAB76116.1; PID:g17133553; GSPDB:GN00179
A; Cross-references: GB:BA000019; PIDN:BAB76116.1; PID:g17133553; GSPDB:GN00179
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                                                                                                                                                                                                                                                                                                     Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70943
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AI2357
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                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence r
A;Molecule type: DNA
A;Residues: 1-300 <COL>
A;Cross-references: GB:AL021899; GB:AL123456;
A;Experimental source: strain H37Rv
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C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: G70943
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S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda,
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Pred. No. 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Geelen, D.; Mergaert, P.; Geremia, R.A.; Goormachtig, S.; van Montagu, M.; Holsters, M Mol. Microbiol. 9, 145-154, 1993
A;Title: Identification of nodSUIJ genes in Nod locus 1 of Azorhizobium caulinodans: evic A;Reference number: 835006; MUID:94018601; PMID:8412659
A;Accession: 835007
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C;Species: Azorhizobium caulinodans
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Feb-2001
C;Accession: S35007
                    C;Date: 30-Sep-2001
C;Accession: JC7681
R;Methner, A.; Leypo
                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 5
A;Introns: 45/1; 88/2; 205/1
C;Superfamily: petunia myb-related protein 1; myb DNA-binding repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myb-related protein-like - Arabidopsis thaliana
N;Alternate names: protein F8M21.200
C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                               RESULT
JC7681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, submitted to the Protein Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 02-Jun-2000 #sequence_revision
C;Accession: T49966
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A; Residues: 1-320 <G
                                                                                     septin 3B - human
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:AL353993; GSPDB:GN00063; ATSP:F8M21.200
A;Experimental source: cultivar Columbia; BAC clone F8M21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
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A; Accession: T49966
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R;Methner, A.; Leypoldt, F.; Jo
Biochem. Biophys. Res. Commun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: ATSP:F8M21.200
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                                                            #sequence_revision 30-Sep-2001 #text_change
F.; Joost,
ommun. 283,
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Pred. No. le+02;
2; Mismatches
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Pred. No. 1e+02;
  P.; Lewerenz,
48-56, 2001
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A;Title: Human septin 3 on chromosome 22q13.2 is upregulated by neuronal differentiation A;Reference number: JC7681; MUID:21222847; PMID:11322766
A;Accession: JC7681
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Result
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Maximum DB seq length: 2000000000
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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SUMMARIES
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MEDLINE=93106233; PubMed=8416818;
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FEBS Lett. 315:85-90(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol.
BASOPHILIC LEUKOCYTES.
SUBUNIT: C3 precursor is first processed by the removal of 4 Arg residues, forming two chains, beta and alpha, linked by a disulfide bond. C3 convertase activates C3 by cleaving the alpha chain, releasing C3A anaphylatoxin and generating C3B (beta chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ent receptor 2.";
280:1277-1281(1998).
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n complement component C3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                      . An amino acid substitution
C3 secretion.";
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ProDom; PD003264; Anaphylatoxin; 1.

PROSITE; SM00104; ANATO; 1.

PROSITE; PS00477; ALPHA 2 MACROGLOBULIN;

PROSITE; PS01177; ANAPHYLATOXIN 1; 1.

PROSITE; PS01178; ANAPHYLATOXIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                              Disease
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005102; F:receptor binding activity; GO; GO:0007186; P:G-protein coupled receptor GO; GO:0006955; P:immune response; TAS. GO; GO:0007165; P:signal transduction; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; K02765; AAA85332.1; -.
PIR; A94065; C3HU.
PDB; 1C3D, 18-NOV-98.
PDB; 1GHQ; 06-JUN-01.
                                                                                                                                                                                                       Complement pathway; Complement alternate pathway; Plasma; Inflammatory response; Glycoprotein; Signal; Polymorphism Disease mutation; 3D-structure; Thioester bond.
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Pfam; PF01835; A2M N; 1.
Pfam; PF01821; ANATO; 1.
Pfam; PF01759; NTR; 1.
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InterPro; IPR001134; Netrin_C.
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InterPro; IPR000020; Anaphylatoxin.
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RELEASED.
- MISCELLANEOUS: I'
TO FORM C3C AND
TO FORM C3G.
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- MISCELLANEOUS: (
AND A COFACTOR )
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DISEASE: Defects in C3 are the cause of C3 deficiency [MIM:120700], that can result in susceptibility to pyogenic infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN. SIMILARITY: Contains 1 anaphylatoxin-like domain.
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        COMPLEMENT C3.
COMPLEMENT C3, ALPH
C3A ANAPHYLATOXIN.
C3B FRAGMENT.
C3DG FRAGMENT.
C3DG FRAGMENT.
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C3D FRAGMENT.
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C1EAVAGE (BY FACTOR
CLEAVAGE (BY FACTOR
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         Y C3 CONVERTASE).
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                                                                                                                                                          ALPHA
                                                                                                                                                                    BETA CHAIN
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protein signalin.
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ANAPHYLATOXIN-LIKE

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Best Local S
Matches 13
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CO3 RABIT
P12247;
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01-OCT-1989
15-SEP-2003
 CARBOHYD
CARBOHYD
SEQUENCE
                                           CHAÎN
CROSSLNK
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequence of cDNA and derived amino acid sequence of rabbit complement component C3 alpha-chain.";
Immunol Invest 15:365-378(1986).

-i- PUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTAGE IS THE CENTRAL REACTION IN BOTH CLASSICAL AND ALTERNATIVE COMPLEMENT PATHWAYS. AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE THIOLESTER, TO CELL SURFACE CARBOHYDRATES OR IMMUNE AGGREGATES.
-i- SUBUNIT: C3 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 ARG RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE BOND. C3 CONVERTASE ACTIVATES C3 BY CLEAVING THE ALPHA CHAIN, RELEASING C3A ANAPHYLATOXIN & GENERATING C3B (BETA CHAIN + ALPHA)
                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                PROSITE; PS01176; ANAPHYLATOXIN 2; PARTIAL.
PROSITE; PS01178; ANAPHYLATOXIN 2; PARTIAL.
PROSITE; PS00477; ALPHA 2 MACROGLOBULIN; 1.
Complement pathway; Complement alternate pathway; Plasma;
Complement pathway; Complement alternate pathway; Plasma;
                                                                                                                                                                                                                       InterPro; IPR000020;
InterPro; IPR001599;
InterPro; IPR001134;
                                                                                                                                                                                                                                                                                  EMBL; M32434; AAA31190.1;
PIR; A27602; A27602.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                send an email to license@isb-sib.ch).
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; PF01759; NTR; 1.
r; SM00643; C345C; 1.
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                                                                                                                                               PS01177; ANAPHYLATOXIN_1; PARTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=3019881;
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Isoglutamyl cysteine thioester (Cys-Gln).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
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Pred. No.
                                                                         COMPLEMENT C3 ALPHA CHAIN.
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EMBL; U55020; AAC49635.1; -.
EMBL; Z75057; CAA99355.1; -.
PIR; 867037; 867037.
SGD; S0005675; SNP3.
GO; GO:0006276; P:plasmid main
InterPro; IRR005599; PMP.
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Q04174; Q09400;
01-OCT-1993 (Rel. 27, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
                                                                                                                                    TRANSMEM CONFLICT
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Tarassov I.A., Winsor B.,
Submitted (MAY-1996) to th
                                                                                                                                                                                 TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mutations in a Saccharomyces cerevisiae host showing holding stability of the heterologous plasmid pSR1."; mol. Gen. Genet. 225:257-265(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ii A., Bordonne R., Camasses A., Madania A., Poch O., assov I.A., Winsor B., Martin R.P.; inted (MAY-1996) to the MBL/GenBank/DDBJ databases FUNCTION: ESSENTIAL PROTEIN INVOLVED IN PLASMID MAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ITHRIHWESASLL 13
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S.POMBE SPAC4G8.12C.
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Pred. No.
  Score 44;
                                               8D8404622CB69534 CRC64;
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Length 516;
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HUMAN
RT09_F
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buecow K.H., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenky Y., Bouffard G.G.,
Blakkelov R. W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003
28-FEB-2003
15-SEP-2003
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-leng-
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                           TRANSIT
CHAIN
                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   Koc E.C., Burkhart W., Blackburn K., Moseley A., Sp. "The small subunit of the mammalian mitochondrial identification of the full complement of ribosomal J. Biol. Chem. 276:19363-19374 (2001).
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                                       SEQUENCE
                                                                                                                                                        Ptam; PF00380; Ribosomal
                                                                                                                                                                    EMBL; BF034318; -; NOT ANNOTATED CDS.
InterPro; IPR000754; Ribosomal_S9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21276436; PubMed=11279123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                              Ribosomal
                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE S9P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DENTIFICATION
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                                                                                                                PD001627; Ribosomal_S9; 1.
; PS00360; RIBOSOMAL_S9; 1.
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Chordata; C
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                                                                                                Mitochondrion;
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   57.1%;
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Last annotation update)
S9, mitochondrial precursor (MRP-S9)
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                                     MITOCHONDRION (POTE 28S RIBOSOMAL PROTE A4ECC6FD3F7FE9AE
   Score
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                                                   1.
1. Transit peptide.
1. Transit peptide.
1. Portion (POTENTIAL).
2. Portion (POTENTIAL)
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 Length 396;
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l_ribosome:
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28-FEB-2003
                                                                             Oxidoreductase;
                                                                                                                                                                                                                                 HSSP; P36234;
                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=WM88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metcalf W.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=316;
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   336
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This SWISS-PROT entry is copyright. It is produce between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There is use by non-profit institutions as long as is modified and this statement is not removed. Use entities requires a license agreement (See http
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- EURZYME REGULATION: Inhibited by NaCl, NADH and sulfite.
-!- SUBUNIT: Homodimer.
-!- INDUCTION: By phosphate starvation.
-!- MASS SPECTROMETRY: MW=36413; MW_ERR=18; METHOD=MALDI.
-!- MISCELLANEOUS: Its optimum pH is between 7.25 and 7.75 and temperature is 35 degrees Celsius.
-!- SIMILARITY: BELONGS TO THE D-ISOMER SPECIFIC 2-HYDROXYACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21264507; PubMed=11278981;
Costas A.M.G., White A.K., Metcalf W.W.;
"Purification and characterization of a novel phosphorus-oxidizing
enzyme from Pseudomonas stutzeri WM88.";
J. Biol. Chem. 276:17429-17436(2001).
                                                                                                    InterPro; IPR006139; 2-Hacid_DH.
InterPro; IPR006140; 2-Hacid_DH_C.
Pfam; PP00389; 2-Hacid_DH; 1.
Pfam; PP02826; 2-Hacid_DH C; 1.
PROSITE; PS00065; D 2 HYDROXYACID_DH_1;
PROSITE; PS00670; D_2-HYDROXYACID_DH_2;
PROSITE; PS00670; D_2-HYDROXYACID_DH_3;
PROSITE; PS00671; D_2-HYDROXYACID_DH_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 276:17429-17430(2002).
-!- FUNCTION: Catalyzes phosphite (phosphonate) oxidation.
-!- CATALYTIC ACTIVITY: Phosphonate + NAD(+) + H(2)O = pho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphonate dehydrogenase (EC 1.20.1.1) (NAD-dependent
                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular genetic analysis of phosphite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99008986; PubMed=9791102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas stutzeri (Pseudomonas perfectomarina)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas stutzeri WM88.";
Bacteriol. 180:5547-5558(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEHYDROGENASES FAMILY.
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(Rel. 41, Last (Rel. 41, Last (Rel. 41, Last (Rel. 41, Last (Rel. 41, Last (Rel. 41))
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7F55D246CA4454F7 CRC64;
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                                                                                                                                                                                                                                           RX Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchett S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchett S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Brotiss R., Boursier C., Ferrari E., Foulger D.,
RA Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Musel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Pessecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffene F.,
Schwiska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Schotin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Yoshida K., Yoshikawa H., Danchin A.,
Thakochi A., Yanamoto H., Yamane K., Yasumoto K., Yata K.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
The Complete genome sequence of the Gram-positive batterium Bacillus
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P94366;
                                                                                                              Nature 390:249-256(1997).
-!- FUNCTION: SOMEHOW INVOLVED RESPIRATION. SEEMS TO BE A
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MEDLINE=97124196; PubMed=8969509;
Yoshida K.-I., Shindo K., Sano H.,
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Zumstein E., Yoshikawa
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InterPro; IPR003593; AAA, ATPase.
InterPro; IPR001140; ABC_TM_transpt.
InterPro; IPR003439; ABC_transporter.
Pfam; PF00664; ABC_membrane; 1.
Pfam; PF00005; ABC_tran; 1.
Problem; PF000006; ABC_transporter; 1.
                                                                                                                                                                    STRAIN=H37Rv;

MEDLINE=982989; PubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd (Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Rutter S., Seeger K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Hypothetical protein Rv1085c.
RV1085C OR MT1117 OR MTV017.38C.
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                                                                                                                            Sulston J.E., Taylor K., Whitehead S., Bar
"Deciphering the biology of Mycobacterium
complete genome sequence.";
Nature 393:537-544(1998).
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., I
Peterson J., DeBoy R., Dodson
                                                  SEQUENCE FROM N.A.
STRAIN=CDC 1551 /
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EMBL; Z99123; CAB15900.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laboratory strains.";
Submitted (APR-2001) to the
-!- SUBCELLULAR LOCATION: Ir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interro.,
Pfam; PF03006; UPruv.,
Pfam; PF03006; hlyIII; 1.
TIGREAMS; TIGRO1065; hlyIII; 1.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; C70895; C70895.
TIGR; MT1117; -.
TubercuList; Rv1085c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                             TISSUE=Breast cancer;
MEDLINE=97462902; PubMed=9323129;
Liu Q., Fischer U., Wang F., Dreyfuss G.;
"The spinal muscular atrophy disease gene product, SMN, and associated protein SIF1 are in a complex with spliceosomal
                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Cre
16-OCT-2001 (Rel. 40, Las
28-FEB-2003 (Rel. 41, Las
Survival of motor neuron
                                                                                                                                                                                                                                                                                          014893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
-:- SIMILARITY: BELONGS TO THE UPF0073 (HLY-III) FAMILY.
                                                                       proteins."
                                                                                                                                                                   NCBI_TaxID=9606
                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                        GEM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bishai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Delcher
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                   interacting pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR004254; HlyIII_related InterPro; IPR005744; HylIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole genome comparison
        SPLICING IN THE NUCLEUS.
SUBUNIT: FORMS A STABLE HETEROMERIC
                                90:1013-1021(1997).
FUNCTION: THE SMN COMPLEX PLAYS
SNRNP ASSEMBLY IN THE CYTOPLASM
                                                                                                                                                                                                                                                                                                        HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL021897; CAA17201.1; -. AE006992; AAK45373.1; -.
                                                                                                                                                                                                                                                                                                                                                                    89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                   ||::|:||:
                                                                                                                                                                                                                                                                                                                                                                                       HRIHWESAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
42 67
67 18
108 15
133 15
159 17
186 20
222 24
 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242
                                                                                                                                                                                                                              (Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
motor neuron protein-interacting
protein 1) (Component of gems 2)
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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K
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87
128
153
179
206
242
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(SMN),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
 GEMIN3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BBC1DE12CF8D3500 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
 BB
                                  AND
 GEMIN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
                                                                                                                                                                                                                                                                                                        280
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                                  ESSENTIAL ROLE IN
           COMPLEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                protein 1 (SMN (Gemin2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 242;
           HTIW
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
           SURVIVAL OF MOTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clinical and
                                                                                             and
                                   V SPLICEOSOMAL PRE-MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration
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RESULT
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Best Local
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01-FEB-1995
01-OCT-1996
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YHM7_
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                                          use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94378003; PubMed=8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dov Johnston M., Andrews S., Brinkman R., Geisel C., Kirsten Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mo Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaug Nhan M., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:10884; SIP1.
GK; 014893; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical YHR067W.
                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P38790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA processing; Spliceosome; Nuclear protein.
DOMAIN 101 106 POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007022; Pfam; PF04938; SIP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF027150; AAB82297.1; -.
                                                                                                                                                                                                                                                          Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                        Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=S288c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                          "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO:0005737; C:cytoplasm; TAS.
GO:0005681; C:spliceosome complex; TAS.
GO:0008248; F:pre-mRNA splicing factor
GO:0008249; P:mRNA processing; TAS.
GO:0000245; P:spliceosome assembly; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: LOCALIZED IN SUBNUCLEAR STRUCTURES COILED BODIES, CALLED GEMS, WHICH ARE HIGHLY ENRICHED IN SPLICEOSOMAL SNRNPS. ALSO FOUND IN THE CYTOPLASM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YEAST
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U00061;
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(Rel.
1 33.1
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  AAB68378.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 1;
Pred. No. 15;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3232F410EA98EB81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                                                        . Usage by and for http://www.isb-sib.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetes;
                                                                                                                                                  restrictions
                                                                                                                                                                             gh a collaboration
EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                     Vaughan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dover J., sten J.,
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Akman L.,
Aksoy S.;
                                                       Complete
INIT_MET
                                                                                                                                              EMBL; AB063521; BAC24157.1; -. HAMAP; MF 00154; -; 1. InterPro; IPR000583; GATase 2. InterPro; IPR005855; Glms. InterPro; IPR001347; SIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=22297718; PubMed=12219091;
MEDLINE=42297718; PubMed=12219091;
MEDLINE=42297718; PubMed=12219091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]
(EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate amidotransferase) (Glucosamine-6-phosphate synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR;
SGD;
                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical
SEQUENCE 2
                                                                                TIGRPAMs; TIGRO1135; glmS; 1.
PROSITE; PS00443; GATASE_TYPE_II; 1.
Transferase; Aminotransferase; Glutamine amidotransferase;
                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                       modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales,
Enterobacteriaceae; Wigglesworthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wigglesworthia glossinidia brevipalpis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLMS OR WIGBR0110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8D3J0;
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     SEQUENCE
                                            NIAMOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            flies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate glutamate + D-glucosamine 6-phosphate.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SIS
                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 1 type-2
                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Catalyzes the first step in hexosamine converting fructose-6P into glucosamine-6P using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   $46699; $46699.
$0001109; YHR067W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 HRIHWD 193
                                                                                                                       PF00310; GATase
PF01380; SIS; 2
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280 AA;
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32:402-407(2002).
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Pred. No.
BY SIMILARITY.
GLUTAMINE AMIDOTRANSFERASE.
GATTASE (BY SIMILARITY).
ISOMERIZATION FRU-6P (BY SIMILARITY),
26571D15AF705AAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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A Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
A Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
A Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
A Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
A Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
A Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
A Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
A Rosenthal A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
A Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
A Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
A Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
A Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
A Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
A Rehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
The DNA sequence of human chromosome 21.";
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16-OCT-2001
15-SEP-2003
 This SWISS-PROT entry is copyright. It is produced through a c
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Mammalia; Eutheria;
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                                             SIMILARITY: Contains 10 immunoglobulin-like C2-type SIMILARITY: Contains 6 fibronectin type III domains.
                                                                            ISOId=060469-2; Sequence=VSP_002502, VTISSUE SPECIFICITY: PRIMARILY EXPRESSED
                                                                                                                                                                                     SUBCELLULAR LOCATION: TYPE I I SHORT ISOFORM MAY BE SECRETED
                                                                                                                                                                                                                 FUNCTION: CELL ADHESION MOLECULE THAT CAN MEDIATE CATION-INDEPENDENT HOMOPHILIC BINDING ACTIVITY. COULD BE INVOLVED NERVOUS SYSTEM DEVELOPMENT.
                                                                                                         Name=Short; Synonyms=CHD2-42
                                                                                                                                                                     ALTERNATIVE PRODUCTS
                                                                                                                        Name=Long; Synonyms=CHD2-52;
IsoId=O60469-1; Sequence=Displayed;
                                                                                                                                                        Event=Alternative splicing; Named isoforms=2
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(Rel. 40, Last sequence update)
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Gellew; normal MIM; 603523; -.

MIM; 603523; -.

GO; GO:0005887; C:integral to plasma membrane; TAS
GO; GO:0005624; C:membrane fraction; TAS.
GO; GO:0007155; P:cell adhesion; TAS.
GO; GO:0007155; P:cell adhesion; TAS.
InterPro; IPR003961; FN III.

InterPro; IPR003961; FN III.

InterPro; IPR003101; Ig-like.
InterPro; IPR003106; Ig-MHC.
R Pfam; PF00041; fn3; 6.
R Pfam; PF00041; fn3; 6.
R Pfam; PF00047; ig; 10.
R SMART; SM00060; FN3; 6.
R SMART; SM00060; FN3; 6.
R SMART; SM00408; IGC2; 7.
R PROSITE; PS50835; IG LIKE; 9.
Immunoglobulin domain; Glycoprotein; Signal; Cel KM Transmembrane; Alternative splicing.
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EMBL; AF023449; AAC17966.1; --
EMBL; AF0217525; AAF27525.1; --
EMBL; AL163283; CAB90446.1; --
EMBL; AL163283; CAB90444.1; --
EMBL; AL163281; CAB90444.1; --
EMBL; AL163281; CCAB90444.1; --
EMBL; AL163281; CCAB90444.1; --
EMBL; AL163281; CCAB90444.1; --
Genew; HGNC: 3039; DSCAM.
MIM; 602523; --
GO; GO:0005624; C:membrane fra
GO; GO:0005687; C:membrane fra
GO; GO:0007155; P:cell adhesic
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DOWN SYNDROME CELL ADHESIO EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 6.

IG-LIKE C2-TYPE 7.

IG-LIKE C2-TYPE 9.

IG-LIKE C2-TYPE 111 1.

IIIINONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 2.

FIBRONECTIN TYPE-III 3.

IG-LIKE C2-TYPE 111 4.

IG-LIKE C2-TYPE 111 5.

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RT "Genome sequence of Yersinia pestis KIM."; RI J. Bacteriol. 184:4601-4611(2002). CC -: FUNCTION: Catalyzes the first step in hexosamine metabolism, CC -: CONVERTING fructose-6p into glucosamine-6P using glutamine as a CC -: CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate = L- CC -: SUBCELLULAR LOCATION: Cytoplasmic (By similarity). CC -: SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SIS FAMILY. CC GFAT SUBPAMILY.	SEQUENCE FROM N.A. STRAIN=KIM5 / Biovar Mediaevalis; STRAIN=22137863; PubMed=12142430; MEDLINE=22137863; PubMed=12142430; Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P. Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.		GLMS_YERPE STANDARD; PRT; 608 AA. ID GLMS_YERPE STANDARD; PRT; 608 AA. AC 082958; DT 28-FEB-2003 (Rel. 41, Last sequence update) DT 28-FEB-2003 (Rel. 41, Last annotation update) DT 2	Query Match 54.3%; Score 38; DB 1; Length 2012; Best Local Similarity 45.5%; Pred. No. 1.3e+02; Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps Qy 1 ITHRIHWESAS 11 Qy : : : : Db 1702 VTHTVHYQSVS 1712	YD 1160 1160 N-LINKED (GLCNAC) (POTE YD 1250 N-LINKED (GLCNAC) (POTE YD 1271 1271 N-LINKED (GLCNAC) (POTE YD 1341 1341 N-LINKED (GLCNAC) (POTE YD 1348 1488 N-LINKED (GLCNAC) (POTE YD 1488 1488 N-LINKED (GLCNAC) (POTE YD 1562 1571 NEWTLNYDGS -> KEAARCKEFS (in Short). (FTId=VSP 002502. /FTId=VSP 002503. (FTId=VSP 002503. HREGDIHLDPYLARDFLANGGEGTSR RTLKRFVLEPIPMEAASSASTREGG GRAELGQAAKMSSSQESLLDSRGHLKGN IGQVTSYICLHTLEWTFC (IN REF. GLAELGQAAKMSSSQESLLDSRGHLKGN IGGVTSYICLHTLEWTFC (IN REF. GLAELGQAAKMSSQESLLDSRGHLKGN IGGVTSYICLHTLEWTFC (IN REF. GLAELGQAAKMSSQUESLLDSRGHLKGN IGGVTSYICLHTLEWTFC (IN REF. GLAELGQAAKMSSQUESLDSRGHLKGN IGGVTSYICHTLEWTFC (IN REF. GLAELGQAAKMSSQUESLDSRGHLKGN IGGVTSYICHTLEWTFT (IN REF. GLAELGQAAKMSSQUESLDSRGHLKGN IGGVTSYICHT (IN REF. GLAELG
			Ф	0,	v 72 %

SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.

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PRT1_PICAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1989
01-OCT-1989
28-FEB-2003
                                                                                                                                                                                                                                               STRAIN=CBS 4732;
STRAIN=EBS 4732;
MEDLINE=89287321; PubMed=2500147;
                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                  EMBL; X15111; CAA33
PIR; S16511; S16511
                                                                                                                                                                                                Hansenula polymorpha.";
Biochim. Biophys. Acta
                                                                                                                                                                                                                                                                                                                                  Saccharomycetales;
NCBI_TaxID=4905;
                                                                                                                                                                                                                                                                                                                                                                Pichia angusta (Yeast) (Hansenula polymorpha).
Eukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP, MF 00164; ; 1.
InterPro; IPR000583; GAMTase_2.
InterPro; IPR005855; GlmS.
InterPro; IPR001347; SIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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PROSITE; PS00443; GATASE_TYPE_II; 1.
Transferase; Aminotransferase; Glutamine amidotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00310; GATase_2; 1. Pfam; PF01380; SIS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; AB0500; AB0500.
                                                                                                                                                                                                                         "Cloning and sequencing of the peroxisomal amine oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT1_PICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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IPR000504; RNA_rec_mot
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(Rel. 12, Last sequence up)
(Rel. 41, Last annotation)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                 CAA33208.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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1
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                                                                                                                                                                                                                                                          Waterham H.R.,
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Pred. No. 42;
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GLUTAMINE AMIDOTRANSFERASE.
GATASE (BY SIMILARITY).
ISOMERIZATION FRU-6P (BY SIMILARITY).
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RESULT 15
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Survival of motor neuron protein-interacting
                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. Uentities requires a license agreement (See htteres)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Sprague-Dawley;
Kallenbach S., La Bella V., Cisterni C., Pettmann B.;
"SMN interacting protein-1 expression pattern in rat.
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIP1 OR GEMIN2.
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PROSITE; PS00030; RRM_RNP_1;
                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00360; RRM;
                                                                                                                                                                                                                                   Pfam; PF04938; SIP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                 EMBL; AF176072; AAD53287.1;
                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                           bmitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
- FUNCTION: THE SMN COMPLEX PLAYS AN ESSENTIAL ROLE IN SPLICEOSOMAL SNRNP ASSEMBLY IN THE CYTOPLASM, AND IS REQUIRED FOR PRE-MRNA SPLICING IN THE NUCLEUS (BY SIMILARITY).
- SUBUNIT: FORMS A STABLE HETEROMERIC COMPLEX WITH SURVIVAL OF MOTOR NEURON PROTEIN (SNN), GEMIN3 AND GEMIN4 (BY SIMILARITY).
- SUBCELLULAR LOCATION: LOCALIZED IN SUBDUCLEAR STRUCTURES NEXT TO COILED BODIES, CALLED GEMS, WHICH ARE HIGHLY ENRICHED IN SUBCESSIONAL SNRNPS. ALSO FOUND IN THE COMPANY.
                                                                                                                                                                                                         processing; Spliceosome; IN 90 95
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                                                                                                                                Similarity 6; Conserv
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                                                                          HRNHWKSQQL 118
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24961 MW;
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Rodentia;
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                                                                                                                                                                                          30440 MW;
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    Mismatches

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POLY-GLN.
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                                                                                                                                                 Score 37; DB
Pred. No. 21;
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Pred. No. 17;
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                                                                                                                                                Pred.
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Sciurognathi; Muridae; Murinae; Rat
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                                                                                                                                                                                            E03AB9DBFCCC7EE3 CRC64;
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(Gemin2).
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STANDARD;

PRT;

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                                                          Query Match
Best Local
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harri
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyc
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998)."
                                                                                                                                                                   HAMAP; MF_00185; -; 1.
InterPro; IPR002627; IPPT.
Pfam; PF01715; IPPT; 1.
ProDom; PD004674; IPPT; 1.
TIGRPAMs; TIGR00174; miaA; 1.
Transferase; Nucleotidyltransferase; tRNA processing; ATP-binding;
                                                                                                               Complete proteome.
NP_BIND 8
SEQUENCE 314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole genome comparison of Mycobacterium tube laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ--i- FUNCTION: CATALYZES THE FIRST STEP IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN=CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Gwinn M.L., Haft D., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Salzberg (
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg (
Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula i
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) (I
transferase) (Isopentenyl-diphosphate:tRNA isopentenyltransferase)
                                                                                                                                                                                                                                                                                                                                  EMBL; AE007108; AAK47116.1; -. PIR; F70505; F70505.
                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z98209; CAB10903.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bishai W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria;
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                                                                                                                                                                                                                                                                                        TubercuList; Rv2727c; -.
                                                                                                                                                                                                                                                                                                                TIGR; MT2799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: Isopentenyl diphosphate + tRNA tRNA containing 6-isopentenyladenosine. SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
FUNCTION: CATALYZES THE FIRST STEP IN THE BIOSYNTHESIS OF 2-METHYLTH-O-NG-(DELTA (2)-ISOPENTENYL)-ADENOSINE (MS[2]I[6]A])
ADJACENT TO THE ANTICODON OF SEVERAL TRNA SPECIES (BY SIMILARITY).
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34446 MW;
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                                    Score 37; DB:
Pred. No. 25;
2; Mismatches
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                                                                                                                                   (POTENTIAL)
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                                                                          Length 314;
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Mikula A.,
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RA Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Stagleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Ra Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bonak S.A., WcEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Bosak S.A., WcEwan R.J., Malek J.A., Gunaratne P.H., RA Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E., Jones S.J.M., Warss R.M., Schein J.E., Jones S.J.M., Warss M.A., Schein J.E., Jones S.J.M., Mara M.A., Schein J.E., Jones S.J.M., Marra M.A.; Froc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

1- SUBCELJULAR LOCATION: Integral membrane protein (Probable).

1- SIMILARITY: BELONGS TO THE NONASPANIN (TM95F) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Warner S.J., Luman.
"Evolution of the TM9 F
"Evolution of the TM9 F
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Mammalia; Eutheria;
                                                                                                                                                                                                            InterPro; IPR004240; EMP70. Pfam; PF02990; EMP70; 1.
                                                                                                                                                                                                                                             EMBL;
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Strausberg R.L., Feingold E.A., Gr
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to the
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Best Local (
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 128-589 FROM N.A.

KAWAKAMI T., Noguchi S., Iroh T., Shigeta K., Senba T., Matsumur Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Obayashi Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugar MISDO human cDNA sequencing project.";

"NEDO human cDNA sequencing project.";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

-i- SUBCELULUAR LOCATION: Integral membrane protein (Probable).

-i- SUBCILULAR LOCATION: ENGRAPANIN (TM9SF) FAMILY.

-i- SIMILARITY: BELONGS TO THE NONASPANIN (TM9SF) FAMILY.

-i- CAUTION: REF 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sugasawa T., Lenzen G., Simon S., Hidaka J., Cahen A., Gulllaume v. Camoin L., Nahmias C., Strosberg A.D.;
"The iodocyanopindolol and SM-11044 binding protein (SMBP) belongs the emerging family of MP70 multispanning membrane proteins.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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HUMAN
                                        EMBL; AF269150; AAF98159.1; -.
EMBL; AF160213; AAF67014.1; ALT_FRAME
EMBL; AF116347; AAF21983.1; -.
EMBL; AK010756; BAA91362.1; ALT_INIT.
InterPro; IPR004240; EMP70.
                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transmembrane 9 superfamily protein member 3
binding protein) (EP70-P-iso)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Adrenal gland;
Gu Y., Peng Y., Li Y.,
Wang Y., Chen Z., Fu G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1999)
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                      PF02990;
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; Primates;
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Pred. No.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
; 22FD4F8588FEC2AE CRC64;
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RESULT 18
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Best Local
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Q00042;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                 SEQUENCE FROM N.A.
STRAIN=K12 / CR63;
Shimizu H., Saitch Y., Suda Y., Uehara K., Sampei G., Mi
"Complete nucleotide sequence of the F plasmid: its impl
organization and diversification of plasmid genomes.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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CONFLICT
                                                                                                                  "Identification of the region that determines the specificity binding of the transposases encoded by Tn3 and gamma delta to terminal inverted repeat sequences.";
Jpn. J. Genet. 69:269-285(1994).
                                                                                                                                                                                                           MEDLINE=95337425; PubMed=7612932; Broom J.E., Hill D.F., Hughes G., Stockwell P.A., Petersen G.B.;
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CHAIN
     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          Enterobacteriaceae;
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
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5:185-189(1995).
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nsposon gamma-delta 80.3 kDa pr
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N-LINKED (GLCNAC. .)
MISSING (IN REF. 2).
M -> I (IN REF. 1).
KYLDPSFFQ -> NILIVLFS (
M -> T (IN REF. 4).
F -> S (IN REF. 4).
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RESULT 19
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Matches 6
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P10193;
01-MAR-1989
FRANSFAC; T0095/; ...
InterPro; IPR001410; DEAD.
InterPro; IPR003450; Hexpes_ori_bp.
Pfam; PF002399; Hexpes_ori_bp; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00487; DEXDC; ATP-binding.
AR ATP (POTENTIAL).
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01-MAR-1989 (Rel. 10,
01-OCT-1996 (Rel. 34,
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                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McGeoch D.J., Dalrymple M.A., Dolan A., McNab D., Taylor P., Challberg M.D., "Structures of herpes simplex virus type 1 genes replication of virus DNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., McNab D., Perry L.J., Scott J.E., Taylor P.; "The complete DNA sequence of the long unique region i herpes simplex virus type 1."; J. Gen. Virol. 69:1531-1574 (1988).
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Alnhaherpesvirinae; Simplexvirus.
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EMBL; M19120; AAA45822.1; -.
PIR; B29890; WMBEU9.
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MEDLINE=88274327; PubMed=2839594;
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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- FUNCTION: PROBABLY INVOLVED IN
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SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL9.
EHV-1 53, AND VZV 51.
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QBWXS8; QBTE55; QBFEB-2003 (Rel
28-FEB-2003 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE=21638061; PubMed=11779638;
Bolz H., Ramirez A., von Brederlow B.,
"Characterization of ADAMTS14, a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADAMTS-14 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 14) (ADAM-TS 14) (ADAM-TS14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
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                                                                                                                                                                                                                                                                 Colige A., Vandenberghe I., Thiry M., Lambert Li S.-W., Prockop D.J., Lapiere C.M., Nusgens "Cloning and characterization of ADAMTS-14, a high homology with ADAMTS-2 and ADAMTS-3."; J. Biol. Chem. 277:5756-5766(2002).
                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 29-1223 FROM N.A. (ISOFORMS B; C ALTERNATIVE PROMOTER USAGE. MEDLINE=21839041; Pubmed=11741898;
                                                                                                                                                                                                                                                                                                                                                                           "Cloning, expression analysis, and structural characteriza
seven novel human ADAWTSs, a family of metalloproteinases
disintegrin and thrombospondin-1 domains.";
Gene 283:49-62(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metalloproteinase family."
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Cal S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Fetal lung;
MEDLINE=21856482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochim. Biophys. Acta 1522:221-225(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                             FUNCTION: Has a aminoprocollagen type I acactivity in the absence of ADAMTS2. Seems latent enzyme that requires activation to
                                                                                                                               alternative promoters;
Event=Alternative splici
                                                                                                                                                                                  matrix (By similarity).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                       peptidase activity.
SUBCELLULAR LOCATION: Secreted.
  TISSUE
                                     Name=D;
                                                                        Name=C;
                                                                                                                                                                      Event=Alternative promoter;
                                             Ime=C;
IsoId=Q8WXS8-3; Se
IsoId=Q8WXS8-4; Sequence=VSI
Note=Produced by alternative
ISSUE SPECIFICITY: Expressed
                                                                                                                                                        Comment=2 isoforms, A
                                                                                                          IsoId=Q8WXS8-1;
                                                                                  IsoId=Q8WXS8-2;
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5; Conserv
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 Sequence=VSP_005501;
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Y: Expressed in retina
                                               Sequence=VSP_006958, VSP_005501; y alternative splicing of isoform
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Pred. No.
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Pfam; PF01562; Pep M12B propep; 1.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF00090; tsp 1; 4.
SMART; SM00209; TSP 1; 4.
SMART; SM00209; TSP 1; 4.
PROSITE; PS00215; ADAM MEDRO; 1.
PROSITE; PS00546; CYSTEINE SWITCH; FALSE NEG.
PROSITE; PS00427; DISINTEGRIN 1; FALSE NEG.
PROSITE; PS00427; DISINTEGRIN 2; FALSE NEG.
PROSITE; PS00142; ZINC_PROTEASE; FALSE NEG.
PROSITE; PS00142; ZINC_PROTEASE; FALSE NEG.
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Anilagen degradation;
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or send a
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InterPro; IPR001590;
InterPro; IPR000884;
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AF366351; AAL79814.1; -.
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Contains 4 TSP type-1 domains.
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RESULT 21
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Maria M., Gren E.D., Dickeon M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickeon M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers
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Nature 393:333-339(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 060895; Q8N1F2;
16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Receptor activity-modifying protein 2 precursor (CRLR activity-modifying-protein 2) (Calcitonin-receptor-like receptor-activity-modifying-protein 2).
                                                       the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by a
                    entities requires a license agreement (
or send an email to license@isb-sib.ch)
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between the Swiss Institute of Bioinformatics and the EMBL
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Mammalia; Eutheria;
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Primates;
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Pred. No. 1.1e+02;
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                                         (See http://www.isb-sib
                                                                                                           There are no restrictions
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Best Local
MEDLINBEZLUGGOGO, MEDLINBEZLUGGOGO, ISDILA K., YOSHINO M., ItOH M., ISDILA I., KAWAI J., Shinagawa A., Fukunishi Y., Komno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Komno H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Fesole G., Quackenbush Schriml L.M., Steaubli F., Suzuki R., Tomita M., Wagner L., Washio Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Lee N.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAH1_MOUSE STANDARD; PRT; 260 AA.

P13634; Q9DC84;

01-JAN-1990 (Rel. 13, Created)

11-FEB-1996 (Rel. 33, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

Carbonic anhydrase I (EC 4.2.1.1) (Carbonate dehydratase
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MOUSE
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CONFLICT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006985; RAMP. Pfam; PF04901; RAMP; 1.
                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUE=Spleen; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser P.J., Cummings P., Curtis P.J. "The mouse carbonic anhydrase I gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90014784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular evolution of the carbonic anhydrase genes: calculation divergence time for mouse carbonic anhydrase I and II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=87169766; PubMed=3104601; Fraser P.J., Curtis P.J.;
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GO:0005887; C:integral to plasma membrane; TA
GO:0005764; C:lysosome; TAS.
GO:0015031; P:protein transport; TAS.
GO:0006898; P:receptor mediated endocytosis;
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BC027975;
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                                                                                                                                                                                                                                                                                                                                         FROM
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6J; TISSUE=Spleen;
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AAH27975.1;
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RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Alleschul S.F., Zeebbrg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Alleschul S.F., Zeebbrg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Alleschul S.F., Zeebbrg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Alleschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Schaefer G.J., Scheetz T.E., RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Robask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Blosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Pahey J., Helton E., Ketteman M., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Ra Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length Br. Proc. Marl Acad. Sci. U.S. A. 99:16809-16603 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S. A. 99:16899-16903 (2002).
-!- FUNCTION: Reversible hydration of carbon dioxide.
-!- CATALYTIC ACTIVITY: H(2) CO(3) = CO(2) + H(2)O.
-!- COFACTOR: Zinc.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUMILARITY: Belongs to the eukaryotic-type carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P. Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilmi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eukaryotic-type carbonic
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EMBL; M32452; AAA37354.1; -.
EMBL; L36655; AAA50291.1; JOINED
EMBL; M28197; AAA50291.1; JOINED
EMBL; L36650; AAA50291.1; JOINED
EMBL; L36651; AAA50291.1; JOINED
EMBL; L36652; AAA50291.1; JOINED
EMBL; L36654; AAA50291.1; JOINED
EMBL; L36654; AAA50291.1; JOINED
EMBL; L36654; AAA50291.1; JOINED
EMBL; AK003066; BAB22544.1; -.
EMBL; BC011233; AAH11233.1; -. METAL CONFLICT EMBL; EMBL; PIR; ; HSSP; METAL SEQUENCE Lyase; Pfam; PF00194; carb_anhydrase; 1.
Probom; PD00085; Euk COanhd; 1.
PROSITE; PS00152; EUK CO2 ANHYDRASE;
Lyase; Zinc; Metal-binding. METAL MGD; MGI:88268; Carl. InterPro; IPR001148; Euk_COanhd. MET A26344; P00915; 1BZM. 119 237 260 A26344. 0 A. 0 94 96 119 237 28189 JOINED.
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JOINED. MW: BY SIMILARITY.
ZINC (CATALYTIC
ZINC) A0C29A7BBBCFEF0C CRC64; (CATALYTIC). P (IN REF. 3 (CATALYTIC) AND 4).

Query Match Best Local Similarity 51.4%; 62.5%; Score 36; Pred. No. ДВ 31; Length 260;

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RESULT
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P48282;
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Mammalia; Eutheria; Ceta
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                     METAL
                                                                                                                                                                                                                                                                                                                Lyase; Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carbonic anhydrase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96251459; PubMed=8690670
Wang L.Q., Baldwin R.L., Jesse B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                   METAL
                                                                                                                                                                                                                                                                                                 METAL
                                                                                                                                                                                                                                                                                                                                         Pfam; PF00194; carb_anhydrase; 1.
ProDom; PD000865; Euk_COanhd; 1.
PROSITE; PS00162; EUK_CO2_ANHYDRASE;
                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001148; Euk COanhd.
Pfam, PF00194; carb_anhydrase; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9940;
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15-SEP-2003
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Belongs to the eukaryotic-type carbonic anhydrase
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ZINC (CATALYTIC).
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cora; Bovoidea;
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Matches
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Q9UHO3;
16-OCT-2001
16-OCT-2001
28-FEB-2003
                                                                                                                                                                                     SEPT3 OR SEP3.
Homo sapiens (Human).
Bukaryota; Metazoa; C
Mammalia; Eutheria; P
Submitted [2]
                 SEQUENCE FROM N.A. (ISOFORMS A AND B).

Methner A., Lewerenz J., Leypoldt F.;

Methier B., Lewerenz J., Leypoldt F.;

Ildentification and characterization of human septin 3 on chromosome 22q13.2 upregulated by retinoic acid induced differentiation of the human neuronal precursor cell line Ntera/D2.";

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00211; ABC_TRANSPORTER_1; FALSE_NEG.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
Nodulation; Membrane; ATP-binding; Transport.
NP BIND 47 ATP (BY SIMILARITY)
SEQUENCE 320 AA; 35310 MW; D89B3BF1E7CC4392 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00005; ABC tran; 1.
ProDom; PD00006; ABC transporter; 1.
ProDom; ANA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the Inthe European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by are entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel.
28-FEB-2003 (Rel.
Neuronal-specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Geelen D.,
                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC_transpo
Pfam; PF00005; ABC_tran; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Membrane-associated.-!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in Nod factor modification.";
Mol. Microbiol. 9:145-154(1993).
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Hyphomicrobiaceae;
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41, Last ann
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Azorhizobium
                                                                                                                                                                                         Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.4%;
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Pred. No.
                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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RA Dunham I, Hunt A.R. (Collins J.E., Bruskiewich R., Beare D.M., A Dunham II, Hunt A.R. (Collins J.E., Bruskiewich R., Beare D.M., A Dunham II, Hunt A.R. (Collins J.E., Bruskiewich R., Babbage A.K., RA Lampun W., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K., RA Bagyuley C., Balkey S.E., Bridgeman A.M., Buck D., Burgess J., Burrill N.D., Eurton J., Carder C., Catter N.P., Chen Y., Clark G., Cleg C., Collier R.E., Connor R., RA Clayg S.M., Cobley V.E., Colle C.G., Collier R.E., Connor R., RA Clayg S.M., Cobley V.E., Colle G.J., Cox A.V., Davis J., Dawson E., Chan Y., Cox P.V., Davis J., Dawson E., Chan Y., Cox P.V., Davis J., Dawson E., Chan Y., Cox P.V., Davis J., Dawson E., Chan P., Cox P.V., Cox P.V., Griffiths M.D., Hall C., RA Chan P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M., RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J., Kingham, A.M., King A., Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M., RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T., A. Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T., RA Marchy J., Mclaren S., McMurray A.A., Milne S.A., Mortinore B.J., Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J., Scott I.G.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L., Ross M.T., Steward C.A., Sulston J.E., Swann R.M., Scott I.E., Swann R.M., Williams L., Williams S.A., Williamson H., Williamson H., Williamson H., Williamson H., Williamson H., Williamson H., Williamson S., Kowasaki K., Sasaki Y., Aoki N., Mitsuyama S., Xudoh J., Shimizu N., Milliamson J., Lewis S., Lin S.-P., Loh P., Malaj E., Nuyren T., Pan H., Lao H.I., Lao
                                                                                                                      EMBL; AP285107; AAG00517.1; -.
EMBL; AP285109; AAG00519.1; -.
EMBL; Z99716; CABA1235.2; ALT_5
PIR; JC7681; JC7681.
                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                       Genew; HGNC:10750; SEPT3.
GO; GO:0016288; P:cytokinesis; NAS
GO; GO:DFR000038; GTP_Cell_Div.
Pfam; PF00735; GTP_CDC; 1.
ProDom; PD002565; GTP_Cell_Div; 1.
                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The DNA sequence of human chromosome Nature 402:489-495(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilkinson P., Boder
Tilahun Y., Wright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20057165;
                                                                                                                                                                                                                                                                                                                                                                                         ISOId=Q9UH03-2; Sequence=VSP 006049; SIMILARITY: BELONGS TO THE SEPTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: INVOLVED IN CYTOKINESIS (POTENTIAL SUBUNIT: MAY ASSEMBLE INTO A MULTICOMPONENT ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=A
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    division;
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55; GTP Cell Div; 1. GTP-binding; Altern
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    Alternative splicing
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                                                                                                                Interpro; IPRO06412; Fruct bisp Calv.

Interpro; IPRO00771; K bp aldolase.

Pfam; PF01116; F bp aldolase; 1.

Probom; P0002376; K bp aldolase; 1.

TIGRFAMs; TIGR01167; cbba; 1.

TIGRFAMs; TIGR01167; cbba; 1.

PROSITE; P500602; ALDOLASE CLASS II 1; 1.

PROSITE; P500602; ALDOLASE CLASS II 2; 1.

PROSITE; P500806; ALDOLASE CLAS
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2_RHOSH
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P29271;
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Fructose-bisphosphate aldolase II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen J.-H., Gibson J.L., McCue L.A., Tabita F.R., "Identification, expression, and deduced primary transketolase and other enzymes encoded within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhodobacteraceae;
NCBI_TaxID=1063;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M68914; AAA26157.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement entities requires a license
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92041881; PubMed=1939098;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; D41080; D41080.
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PATHWAY: PART OF REDUCTIVE PENTOSE PHOSPHATE PATHWAY OR CALVIN CYCLE OF PHOTOSYNTHETIC CARBON DIOXIDE ASSIMILATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: THIS PROTEIN IS ENCODED WITHIN THE RIBULOSE-BISPHOSPHATE CARBOXYLASE OPERON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way fied and this statement is not removed. Usage by and for commercial ties requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Belongs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 VTHNIHYET 310
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                                                                                                   354 AA;
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lase II (EC 4.1.2.13).
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or send a
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InterPro; IPR000038; GTP Cell Div.
Pfam; PF00735; GTP CDC; I.
ProDom; PD002565; GTP Cell Div; 1.
Cell division; GTP-binding.
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   MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka
Miyajima N., Hirosawa M., Sugiura M.,
                                                                                                                                                                                           Synechocystis sp. (strair Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                            Gamma-glutamyltranspeptidase precursor GGT OR SLR1269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Promoter-trap insertion into a novel mammalian septin g during mouse neuronal development."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                        01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kiong J.-W., Stuhlmann H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: INVOLVED IN CYTOKINESIS (POTENTIAL).
SUBUNIT: MAY ASSEMBLE INTO A MULTICOMPONENT STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buropean Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE SEPTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF104411; AAD02884.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITHRIHWES 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSHMAHWVGASV 139
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(Rel. 35,
(Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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52791 MW;
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55.6%;
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; 13E89DC80971382A CRC64;
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Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Sciurognathi; Muridae;
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r (EC 2.
A., Asamizu E., Naka
Sasamoto S., Kimura
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                                                                                                                                                                                              Synechocystis
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; Murinae; Mus
                             Nakamura Y.,
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                     MEDLINE=96121379; PubMed=8575760;
Vyas P., Vickers M.A., Picketts D.J., Higgs D.
"Conservation of position and sequence of a no
gene containing the major human alpha-globin r
Genomics 29:679-689(1995).
                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamada M., Yasuda M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."
DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: (5-L-glutamyl)-peptide + an amino acid = peptide + 5-L-glutamyl-amino acid.
peptide + 5-L-glutamyl-amino acid.
-!- PATHWAY: GGT PLAYS A KEY ROLE IN THE GAMMA-GLUTAMYL CYCLE, A PATHWAY FOR THE SYNTHESIS AND DEGRADATION OF GLUTATHIONE.
-!- SUBUNIT: THIS ENZYME CONSISTS OF TWO POLYPEPTIDE CHAINS, WHIC SYNTHESIZED IN PRECURSOR FORM A SINGLE POLYPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                 CGTHBA.
                                                                                                                                                                                                                                                                                                                                                                                        CGTHBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS; TIGRO0066; g_glut_trans; 1.
PROSITE; PS00462; G_GLU_TRANSPEPTIDASE; FALSE_NEG
Transferase; Acyltransferase; Zymogen; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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PRINTS; PR01210; GGTRANSPTASE.
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Shimpo S., Takeuchi C.,
                                                                                                                                                                                                                                                                                                                                     (Human)
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Primates;
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Pred. No.
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                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
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Wada T., Watanabe /
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                                                                                                                 novel, widely expressed
n regulatory element.";
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Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases

SEQUENCE

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RESULT 30
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28-FEB-2003
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                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsit the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentials requires a license agreement (See http://www.isb-sib.ch/ar
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EMBL; AE014078; AAM67598.1; -. HAMAP; MF 00164; -; 1. InterPro; IPR000583; GATase_2. InterPro; IPR001347; SIS.
                                                                                                                                                             entities re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "50 million years of genomic stasis in endosymbiotic Science 296:2376-2379(2002).
-!- FUNCTION: Catalyzes the first step in hexosamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S., Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.; "50 million years of genomic stasis in endosymbiotic bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amidotransferase) (Glucosamine-6-phosphate synthase).
GLMS OR BUSG027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-phosphate phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Last annotation update)
Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                             converting fructose-6P into glucosamine-6P using g nitrogen source (By similarity).

CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-pho glutamate + D-glucosamine 6-phosphate.

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: Widely expressed.
SIMILARITY: BELONGS TO THE UPF0171 FAMILY.
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NCE 569 AA; 636
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                                                                                                                                                          equires a license agreement (Semail to license@isb-sib.ch).
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(Rel. 41,
(Rel. 41,
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Pred. No.
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                                                                                                                                                                                   noved. Usage by and for commercial
  (See http://www.isb-sib.ch/announce/
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Matches 5
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Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
Nature 407:81-86(2000).
-!- FUNCTION: CATALYZES THE FIRST STEP IN HEXOSAMINE METABOLISM,
CONVERTING FRUCTOSES 6P INTO GLUCOSAMINE-6P USING GLUTAMINE AS
NITROGEN SOURCE (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate = L-
glutamate + D-glucosamine 6-phosphate.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SIS FAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]
(EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GPAT) (L-glutamine-D-fructose-6-phosphate amidotransferase) (Glucosamine-6-phosphate synthase).
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P57138;
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            HAMAP; MF_00164; -; 1.
InterPro; IPR000583; GATase_2.
InterPro; IPR00585; GlmS.
InterPro; IPR001347; SIS.
Pfam; PF00310; GATase_2; 1.
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                                                                                                      HSSP; P17169; 1
                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Tokyo 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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INIT_MET 0
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PROSITE; PS00443; GATASE_TYPE_II; 1.
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Pfam; PF01380; SIS; 2
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                                                                                       MEROPS;
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5; Conserv
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                                                                                                                                                   equires a license agreement (email to license@isb-sib.ch)
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62.5%;
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GLUTAMINE AMIDOTRANSFERASE.
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
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Pred. No.
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GATase_2; 1. SIS; 2.

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RESULT 32
T9S4_HUMA
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Deloukas P., Matthews L.H., Ashurst J., Bardon J.K., Bagguley C.L.,
RA Bailey J., Barlow K.E., Bates K.N., Beard L.M., Beare D.M.,
RA Bailey J., Barlow K.E., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.B., Corby N.R.,
RA Cliston A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Frasgr A., French L., Garner P.,
RA Ellington A.G., Frankland J.A., Frasgr A., French L., Garner P.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howlor S.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Phillimore B.J. C.T., Patel R., Pearce T.A.V., Peck A.I.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Wilneing J.., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Wiltehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Milneing J.., Wary P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Milneing J.., Wary P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohara O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q92544; Q9NUA3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21638749; PubMed=11780052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.; "Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain."; DNA Res. 3:321-329(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   analysis
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               NA sequence and comparative analysis of human chromosome 414:865-871(2001).
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5; Conserv
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PS00443; GATASE_TYPE_II; 1.
se; Aminotransferase; Gluta
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Seki N., Ishikawa K.-I
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family protein member 4.
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GATASE (BY SIMILARITY).
ISOMBRIZATION PRU-6P (BY SIMILARITY).
GLUTAMINE AMIDOTRANSFERASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ., Ohira M.,
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. 78;
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Bakesley R.W., Touchman J.W., Green E.D., Dickson, M.C.,

Balakesley R.W., Touchman J.W., Green E.D., Dickson, M.C.,

Balakesley R.W., Touchman J.W., Green E.D., Dickson, M.C.,

Balakesley R.W., Touchman J.W., Green E.D., Dickson, M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Balakesley R.W., Touchman J.W., Green E.D., Dickson, M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerch A., Schein J.S., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

"Unman and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                      - VAV RAT
P54100;
01-OCT-1996
01-OCT-1996
15-SEP-2003
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
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                                                                             VAV1 OR VAV.
                                                                                               Vav proto-oncogene
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    -!- SUBCELLULAR LOCATION: Integral membrane protein (Prob-
    -!- SIMILARITY: BELONGS TO THE NONASPANIN (TM9SF) FAMILY.

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TYSVHWEESDI 244
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AAH22850.1;
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Chordata;
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4; Mismatches
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Craniata; Vert
Sciurognathi;
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Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Rat
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PRINTS; PROUGUS; SH3; 2.

PRINTS; PROUGUS; SH3DOMAIN.

PRINTS; PROUGUS; SH3DOMAIN.

PRINTS; PROUGUS; SM22CALPONIN.

PRODOM; PDOUGUS; CH type; 1.

ProDom; PD0001527; CH type; 1.

ProDom; PD000066; SH3; 1.

PRODOM; PD0000066; SH3; 1.

SMART; SM00109; C1; 1.

SMART; SM00109; C1; 1.

SMART; SM000325; RhoGEF; 1.

SMART; SM00325; SH3; 2.

SMART; SM00325; SH3; 2.

SMART; SM00326; SH3; 2.

SMART; SM00253; SH3; 2.

PROSITE; PS50021; CH; 1.

PROSITE; PS50010; DAG_PE_BIND_DOM
PROSITE; PS50010; DH Z; 1.

PROSITE; PS50001; DAG_PE_BIND_DOM
PROSITE; PS50001; DH_DOMAIN; 1.

PROSITE; PS50001; SH3; 2.

PROSITE; PS50001; SH3; 2.

PROSITE; PS50001; SH3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001715; Calponin-like.
InterPro; IPR003247; CH type.
InterPro; IPR0032219; DAG PE-bind.
InterPro; IPR001331; GDS CDC24.
InterPro; IPR001849; PH-
InterPro; IPR001849; Rh-GEF.
InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
InterPro; IPR001452; SH3.
InterPro; IPR001096; SM22 calponin.
InterPro; IPR001096; SM22 calponin.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00307; CH; 1.
Pfam; PF00130; DAG PE-bind
Pfam; PF00169; PH; 1.
Pfam; PF000621; RhoGEF; 1.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 2.
Proto-oncogene; Phorbol-ester binding; Zinc; Guanine-nucleotide releasing factor; Repeat; DOMAIN 119 CH.

DOMAIN 194 373 DH.

DOMAIN 194 373 DH.

DOMAIN 402 504 PHORBOL-ESTER AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U39476; AAA98606.1; -.
HSSP; P29354; 1GRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <del>-</del> <del>-</del> <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Song J.S., Haleem-Smith H., Arudchandran R., Gome Mill J.F., Tan T.-H., Rivera J.;
"Tyrosine phosphorylation of Vav stimulates IL-6 cells by a Rac/c-Jun N-terminal kinase-dependent J. Immunol. 163:802-810(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM MEDLINE=993:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: Phosphorylated on tyrosine residues.
SIMILARITY: Contains 1 calponin-homology (CH) domain.
SIMILARITY: Contains 1 DBL-homology (DH) domain.
SIMILARITY: Contains 1 PH domain.
SIMILARITY: Contains 1 zinc-dependent phorbol-ester and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a capen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 1 SH2 domain. SIMILARITY: Contains 2 SH3 domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the Rho/Rac GTPases, thus leading to cell di
proliferation.
SUBUNIT: Interacts with SLA (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Couples tyrosine kinase signals with the activation of the Rho/Rac GTPases, thus leading to cell differentiation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PE-bind;
                                                                                                                                                                                _DOM_2;
 PHORBOL-ESTER AND DAG BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Usage by
                                                                SH2 domain; SH3 domain; Phosphorylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   production
pathway.";
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VAV MOUSE

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Best Local
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                                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proliferation.
-!- SUBUNIT: Interacts with SLA.
-!- TISSUE SPECIFICITY: Widely expressed in hematopoietic cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILINE 20130290; PubMed=10662792;
Sosinowski T., Pandey A., Dixit V.M.,
"Src-like adaptor protein (SLAP) is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-93 FROM N.A.

MEDLINE=91172176; PubMed=2005887;

Katzav S., Cleveland J.L., Heslop H.E., Pulido D.;

Katzav S., Cleveland J.L., Heslop H.E., Pulido D.;

"Loss of the amino-terminal helix-loop-helix domain oncogene activates its transforming potential.";

mol. Cell. Biol. 11:1912-1920(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=92228488; PubMed=1565462;

Adams J.A., Houston H., Allen J., Lints T., Harvey R

Adams J.A., Houston H., Allen J., Lints T., Harvey R

"The hematopoietically expressed vav proto-oncogene

with the dbl GDP-GTP exchange factor, the bcr gene a

(CDC24) involved in cytoskeletal organization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vav proto-oncogene VAV1 OR VAV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor signaling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTION WITH SLA.
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                                                                                                                                                                                                                                                                                                        FUNCTION: Couples tyrosine kinase the Rho/Rac GTPases, thus leading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                not in other cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
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SH3 2.
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Pred. No. 1.1e
3; Mismatches
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Sciurognathi; Muridae; Murinae; Mus
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negative 1
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EMBL; X64361; CAA45713.1;

ch/announce,

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A61187; 1F5X; 1

15-SEP-00

VASWAL

M59833;

AAA63402.1;

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ID NAV3
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                                                               RESULT
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                                                                                                                                                                 Query Match
Best Local S
Matches 5
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PROSITE; PS00479; DAG PE_BIND_DOM_1; 1.

PROSITE; PS50001; DAG PE_BIND_DOM_2; 1.

PROSITE; PS50010; DH_2; 1.

PROSITE; PS5000741; DH_1; 1.

PROSITE; PS50003; PH_DOMAIN; 1.

PROSITE; PS50001; SH3; 1.

PROSITE; PS50002; SH3; 2.
      "3_HUMAN STANDARD;

VAV3_HUMAN STANDARD;

Q9UKW4; O95230; Q9Y5X8;

16-OCT-2001 (Rel. 40, Cre

16-OCT-2001 (Rel. 40, Las

28-FEB-2003 (Rel. 41, Las
                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 2.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00888; SM22CALPONIN.
PRODom; PD001527; CH type; 1.
ProDom; PD001093; SH3; 1.
ProDom; PD000066; SH3; 1.
                                                                                                                                                               DOMAIN
CONFLICT
SEQUENCE
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DOMAIN
DOMAIN
DOMAIN
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SMART;
SMART;
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Pfam; PF00130; DAG PE-bind; 1.
Pfam; PF00169; PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                  SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
InterPro; IPR003096; SM22_calponin.
                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                             Juanine-nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001715; Calponin-like.
InterPro; IPR003247; CH_type.
InterPro; IPR003219; DAG PE-bind.
InterPro; IPR001331; GDS CDC24.
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                                                                                                                                                                                                                                                  D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:98923;
                                                                                                                                                                                                                                                                                                                                                     ; SM00233; PH; 1.
; SM00325; RhoGEF; 1.
; SM00252; SH2; 1.
; SM00326; SH3; 2.
protein.
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SM00033; CH;
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5; Conserv
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                                            STANDARD;
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SM22CALPONIN.
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373
504
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660
765
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annotation updat
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DH.
PH.
PH.
SH3 1.
SH2.
SH3 2.
SH3 2.
Q -> E (IN REF. 2).
MW; 3666DCCD1C5229DA CRC64;
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                                                                                                                           Score 36; DB 1; Length 845;
Pred. No. 1.1e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                            factor;
                                                                                                                                                                                                                                                           binding; Zinc;
factor; Repeat;
                                            847
                                            B
                                                                                                                                                                                                                                                           SH2 domain; SH3 domain; Phosphorylation;
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GO; GO:0005096; F:GTPase activator activity; TAS.
GO; GO:0005070, F:SH3/SH2 adaptor protein activity; TAS
GO; GO:0007264; P:SH3/SH2 adaptor protein activity; TAS
GO; GO:0007264; P:small GTPase mediated signal transduc
InterPro; IPR001715; Calponin-like.
InterPro; IPR003247; CH type.
InterPro; IPR003247; CH type.
InterPro; IPR001331; GDS_CDC24.
InterPro; IPR001331; GDS_CDC24.
InterPro; IPR001849; PH.
InterPro; IPR000219; RhoGEF.
InterPro; IPR000219; RhoGEF.
InterPro; IPR000980; SH2.
InterPro; IPR000980; SH2.
InterPro; IPR00196; SM22_calponin.
Pfam; PP00307; CH; 1.
Pfam; PP00307; CH; 1.
                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF118887; AAD20349.:
EMBL; AF118886; AAD20348.:
EMBL; AF067817; AAC79695.:
HSSP; P29355; 1SEM.
Genew; HGNC:12659; VAV3.
MIM; 605541; -
             Pfam; PF
PRINTS;
PRINTS;
PRINTS;
PRODOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trenkle T., Welsh J., Jung B., Mathieu-Daude F., McClelland M.;
"Non-stoichiometric reduced complexity probes for cDNA arrays.";
Nucleic Acids Res. 26:3883-3891(1998).

-i- FUNCTION: EXCHANGE FACTOR FOR GTP-BINDING PROTEINS RHOA, RHOG AND,
-IO A LESSER EXTENT, RAC-1. BINDS PHYSICALLY TO THE NUCLEOTIDE-FREE STRIES OF THOSE GTPASES.
-I- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                               Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND ALTERNATIVE SP
MEDLINE=99455043; PubMed=10523675;
MOVILLA N., Bustelo X.R.;
"Biological and regulatory properties
Vav family of oncoproteins.";
Mol. Cell. Biol. 19:7870-7885(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Breast, and MEDLINE=98371222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                binding domain.
SIMILARITY: Contains 1 SH2 domain.
SIMILARITY: Contains 2 SH3 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId-Q9UKW4-2; Sequence=VSP_001820;
SIMILARITY: Contains 1 calponin-homology (CH) domain.
SIMILARITY: Contains 1 DBL-homology (DH) domain.
SIMILARITY: Contains 1 PH domain.
SIMILARITY: Contains 1 zinc-dependent phorbol-ester and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Beta;
                                                                                                            PF00169; PH; 1.
PF00621; RhoGEF; 1.
                                                                               PF00017; SH2; 1. PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9UKW4-1;
                             PR00401; SH2DOMAIN.
PR00452; SH3DOMAIN.
PR00888; SM22CALPONIN.
 PD001527;
                                                                                                                           0; DAG_PE-bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            ; AAD20349.1; -.; AAD20348.1; -.; AAC79695.1; -.
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CH_type; 1.
SH2; 1.
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PubMed=9705494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                               signal transduction; TAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      new member of the
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PD000066;

SH3;

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                                               MEDLINE=20179693; PubMed=10713454;

MEDLINE=20179693; PubMed=10713454;

MITTERKLE T., McClelland M., Adlkofer K., Welsh J.;

Major transcript variants of VAV3, a new member of the VA

Major transcript variants of rew member of the VA

Gene 245:139-149(2000).

C -:- FUNCTION: EXCHANGE FACTOR FOR GTP-BINDING PROTEINS RHC

C -:- FUNCTION: EXCHANGE FACTOR FOR GTP-BINDING PROTEINS RHC

C TO A LESSER EXTENT, RAC-1. BINDS PHYSICALLY TO THE NUC

STATES OF THOSE GTPASES (BY SIMILARITY).

C -:- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 5
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SMART; SM000233; PH; 1.

SMART; SM00025; RhoGEF; 1.

SMART; SM000325; SH2; 1.

SMART; SM000326; SH3; 2.

PROSITE; PS500021; CH; 1.

PROSITE; PS5000479; DAG_PE_BIND_DOM_1; 1.

PROSITE; PS50001; DH_2; T.

PROSITE; PS50010; DH_2; T.

PROSITE; PS50010; DH_2; T.

PROSITE; PS50003; PH_DOMAIN; 1.

PROSITE; PS50003; PH_DOMAIN; 1.

PROSITE; PS50001; SH2; 1.

PROSITE; PS50002; SH3; 2.

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DOMAIN 192 3

DOMAIN 400 5

DOMAIN 514 5

DOMAIN 592 6

DOMAIN 672 7

DOMAIN 788 8

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SMART; S
                                                                                                                                                                                            Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                     VAV3.
                                                                                                                                                                                                                                              Vav-3 protein.
                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40, 15-SEP-2003 (Rel. 42,
                                                                                                                                                                                                                                                                                             Q9R0CB;
                                              Event=Alternative
                                                                                                                                                                                       _TaxID=10090;
                                                                                                                                                                                                                                                                                                        MOUSE
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SM00033; CH; 1.

SM00233; PH; 1.

SM00235; RhOGEF; 1.

SM00325; SH2; 1.

SM00326; SH3; 2.
                                                                                                                                                                                                                                                                                                                                                                  21
IsoId=Q9R0C8-2;
                       IsoId=Q9R0C8-1;
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217
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Last sequence update)
Last annotation updat
                       Sequence=Displayed;
 Sequence=Not described
                                              splicing; Named isoforms=2;
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3; Mismatches
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SH3 1.
SH2.
SH3 2.
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LLCQLLNNLRAHSINLKEINLRPQMSQFLCLKNIRTFLTAC
CETFGMRKSELFEAFDLFDVRDFGK -> MQLEDCPCRAHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor;
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H (IN REF. 1; AAD20348).

S (IN REF. 2).

A (IN REF. 1; AAD20348).
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1.1e+02;
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tive splicing.
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ProDom; PD000093; SHZ; 1.

ProDom; PD0000066; SH3; 1.

SMART; SM00109; C1; 1.

SMART; SM00013; CH; 1.

SMART; SM00233; PH; 1.

SMART; SM00233; PH; 1.

SMART; SM00252; SH2; 1.

SMART; SM00252; SH2; 1.

SMART; SM00252; SH3; 2.

SMART; SM00252; SH3; 2.

PROSITE; PS00021; CH; 1.

PROSITE; PS000479; DAG_PE_BIND_DOM_1; 1.

PROSITE; PS00010; DHG_PE_BIND_DOM_2; 1.

PROSITE; PS00001; SH3; 2.

PROSITE; PS00001; SH3; 2.

PROSITE; PS00001; SH3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001/15; Calponin-like.
InterPro; IPR003247; CH type.
InterPro; IPR003247; CH type.
InterPro; IPR002219; DAG_PE-bind.
InterPro; IPR001331; GDS_CDC24.
InterPro; IPR001849; PH.
InterPro; IPR000219; RhoGEF.
InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
InterPro; IPR001452; SH3.
InterPro; IPR003096; SM22_calponin.
Pfam; PF003007; CH; 1.
Pfam; PF00130; DAG_PE-bind; 1.
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-!- SIMILARITY: Contains 2 s.
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Pfam; PF00621; RhoGEF; 1.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                      Guanine-nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF067816; AAF09171.1; -.
                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                     ; PR00401; SH2DOMAIN.; PR00452; SH3DOMAIN.; PR00885; SM22CALPONIN.; PR00885; CH type; 1.; PD000093; SH2; 1.; PD000066; SH3; 1.
                       w
                                               Similarity
5; Conserv
HRVTWDSAQV
                      HRIHWESASL
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                                                Conservative
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                                                           50.0%;
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1 DBL-homology (DH)
1 PH domain.
1 zinc-dependent pho
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SH3
                                                                                              py SH2 domain; SH3 domain; Reging factor; Alternative splicing the ph.

DH.

PH.

PH.

PHORBOL-ESTER AND DAG BIND1 SH3 1.

SH2.

SH3 2.

SH3 2.
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                                               Score 36; DB 1; Li
Pred. No. 1.1e+02;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domains
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                                                                                                                                                                                                  domain; SH3 domain; Repeat; tor; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phorbol-ester and
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                                                                        Length 847;
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restrictions of
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L outstation -
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                                                Gaps
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PESTROGEN regulation of tissue-specific expression of complement C3.";

J. Biol. Chem. 264:16947[1989].

C. -i- FUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL CC REACTION IN BOTH CLASSICAL AND ALTERNATIVE COMPLEMENT PATHWAYS.

C. AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE THIOLESTER, TO CELL SURFACE CARBOHYDRATES OR IMMUNE AGGREGATES.

C. -I- FUNCTION: DERIVED FROM PROTECLYTIC DEGRAPATION OF COMPLEMENT C3, C2.

C. -I- FUNCTION: DERIVED FROM PROTECLYTIC DEGRAPATION OF COMPLEMENT C3, C3.

C. C-I- FUNCTION: DERIVED FROM PROTECLYTIC DEGRAPATION OF COMPLEMENT C3, C3.

C. C-I- SUBULITIES CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND C3.

C. SUBUNIT: C3 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 ARG RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE BOND. C3 CONVERTASE ACTIVATES C3 BY CLEAVING THE ALPHA CHAIN, RELEASING C3A ANAPHYLATOXIN & GENERATING C3B (BETA CHAIN + ALPHA)
                          EMBL; X52477; CAA36716.1; ---
EMBL; M99866; AAA40837.1; ALT_SEQ.
PIR; S15764; C3RT.
PDB; 1QOP; 31-JUL-00.
PDB; 1QOP; 31-JUL-00.
InterPro; IPR000280; A2M N.
InterPro; IPR000200; Anaphylatoxin.
InterPro; IPR000159; MacrogloblnA2.
InterPro; IPR000134; Netrin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CO3_RAT
P01026;
                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as not removed. and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                         This SWISS-PR
between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=79062262; PubMed=309768; Jacobs J.W., Rubin J.S., Hugli T.E., Bogardt Daniels J.S., Daughaday W.H., Bradshaw R.A.; "Purification, characterization, and amino ac anaphylatoxin (C3a)."; Biochemistry 17:5031-5038(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990 (Rel. 15,
15-SEP-2003 (Rel. 42,
Complement C3 precurse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 671-748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misumi Y., Sohda M., Ikehara Y.;
"Nucleotide and deduced amino acid sequence of
Nucleic Acids Res. 18:2178-2178(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Wistar; TISSUE=Liver; MEDLINE=90245672; PubMed=233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
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                   [nterPro; IPRO
Pfam; PF00207;
                                                                                                                                                                                                                                                                                                                                        SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN. SIMILARITY: Contains 1 anaphylatoxin-like domain.
                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor [Contains:
A2M; 1
A2M_N;
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omm B.S., Ponce-De-Leon H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=2336397;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
or [Contains: C3A anaphylatoxin].
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Sciurognathi; Muridae; Murinae; Rattus
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                                                                                                                                                                                                                       http://www.isb-sib.ch/announce/
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POLG_TBEVS
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Best Local S
Matches 7
                                                                                                                                                                      POLG TBEVS STANDARD; PRT; 3412 AA.

PO7720; PO7721; Q88475; Q88476; Q88477; Q88478; Q88479; Q88877;
Q88878; Q88879;
O1-APR-1988 (Rel. 07, Created)
O1-MAY-1991 (Rel. 18, Last sequence update)
O1-MAY-1991 (Rel. 18, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Genome polyprotein [Contains: Capsid protein C (Core protein); |
Genome polyprotein [Contains: capsid protein E, Nonstru
proteins (SI, NSZA, NSZB, NS4A and NS4B; Protease/helicase
(EC 3.4.21.98) (NS3); RNA-directed RNA polymerase (EC 2.7.7.48)
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CHAIN
PEPTIDE
CHAIN
                         Pletnev A.G., Yamshchikov v.r., -
Pletnev A.G., Yamshchikov v.r., -
"Nucleotide sequence of the genom
of the polyprotein of tick-borne
Virology 174:250-263(1990).
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MEDLINE=90101381; PubMed=2136778;
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            SEQUENCE OF 1-1190 FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00477; ALPHA 2 MACROG PROSITE; PS01177; ANAPHYLATOXIN PROSITE; PS01178; ANAPHYLATOXIN
MEDLINE=88319988; PubMed=2970626;
                                                                                                            NCBI_TaxID=11087;
                                                                                                                            Flavivirus
                                                                                                                                     Viruses; seRNA positive-strand
                                                                                                                                                Tick-borne encephalitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
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                                 Yamshchikov V.F., Blinov v.m.; equence of the genome and complete amino acid region of tick-borne encephalitis virus.";
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70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 MACROGLOBULIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C3B (ALPHA' CHAIN).

CLEAVAGE (BY C3 CONVERTASE).

ANAPHYLATOXIN-LIKE.

INTERCHAIN (BY SIMILARITY).

BY SIMILARITY.

                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB
Pred. No. 2.3e
1; Mismatches
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N-LINKED (GLCNAC. . .) (PROBABLE)
N-LINKED (GLCNAC. . .) (PROBABLE)
LK -> KL (IN REF. 2).
MW; 2F87CCB143CDD4BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALPHA CHAIN.
C3A ANAPHYLATOXIN
C3B (ALPHA' CHAIN
                                                                                                                                   (strain Sofjin)
d viruses, no DN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nate pathway; Plasma;
Signal; 3D-structure
                                                                                                                                                                                                                                                                                                                                                                               DB 1;
2.3e+02;
2;
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Y C3 CONVERTASE).
                                                                                                                                       DNA stage;
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E; Nonstructural
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pletnev A.G., Yamshchikov V.F., Blinov V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=86220766;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; S07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor position, CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virion structural proceins.";
S Lett. 200:317-321(1986).
FUNCTION: TUP TOTAL
                                   n; PF01003; Flavi_capSid; 1.

n; PF02832; Flavi_glycop_C;

n; PF00869; Flavi_glycoprot;

n; PF00949; Flavi_helicase; 1

n; PF01004; Flavi_NS1; 1.

n; PF01005; Flavi_NS2A; 1.

n; PF01005; Flavi_NS2A; 1.

n; PF01005; Flavi_NS2B; 1.

n; PF01350; Flavi_NS4A; 1.

n; PF01349; Flavi_NS4B; 1.

n; PF01349; Flavi_NS5; 1.

n; PF01572; Flavi_NS5; 1.

n; PF01728; FtsJ; 1.

n; PF01728; FtsJ; 1.

n; PF01728; FtsJ; 1.

n; PF01728; FtsJ; 1.
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MISCELLANEOUS: THE NONSTRUCTURAL PROTEINS NS1 PRESENTS TWO ALTERNATIVE CLEAVAGE SITES FOR ITS C-TERMINUS, WHICH MAY DEFINE SOLUBLE OR A MEMBRANE-BOUND FORM OF NS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARI HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCT: NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the contract of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             European
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   o; IPRO01410; DEAD.
co; IPRO01122; Flavi_glycopro
pi IPR000336; Flavi_glycopro
pi IPR0001850; Flavi_Melicase
pi IPR000169; Flavi_M.
iPR0001572; Flavi_MS2A.
iPR000477; Flavi_MS2A.
iPR000404; Flavi_MS2B.
iPR000404; Flavi_MS4B.
iPR0002535; Flavi_MS4B.
iPR0002535; Flavi_MS4B.
iPR0002877; Flavi_MS4B.
iPR0002877; Flavi_MS5B.
iPR0002877; Flavi_MS5B.
iPR0002877; Flavi_MS5B.
iPR0002877; Flavi_Dropep.
iPR0002877; Flavi_Dropep.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001650; Helicase C.
IPR007095; RNA pol DS PS.
IPR007094; RNA pol PSvir.
1003; Flavi capsid; 1.
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CAA27502.1;
CAA27503.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVITY: Hydrolyeis of four peptide bonds in the vipolyprotein, commonly with Asp or Glu in the P6 Cys or Thr in P1 and Ser or Ala in P1.

ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAA27505.1;
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_glycoprot; 1.
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i_helicase.
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  (See http://www.isb-sib.ch/announce/
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RESULT 39
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ID WIT1 HUMAN S
AC Q06250; Q96A27;
DT 01-NOV-1995 (Rel
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DISULFID
                                                          TISSUE=Placenta;
MEDLINE=94010952; PubMed=8406502;
Gassler M., Bruns G.A.P.;
"Sequence of the WT1 upstream region
Genomics 17:499-501(1993).
                                                                                                                                                                                                                                                                                             WIT1.
                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel.
28-FEB-2003 (Rel.
15-SEP-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Core protein;
ATP-binding; 7
                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                     Wilms' tumor
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TISSUE=Kidney;
                     SEQUENCE FROM N.A
                                                                                                                                                                                                        NCBI_TaxID=9606;
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40 385
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7 618
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71.4%;
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BY SIMILARITY.

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NONSTRUCTURAL PROTEIN NS
NONSTRUCTURAL PROTEIN NS
PROTEASE/HELICASE (NS3).
NONSTRUCTURAL PROTEIN NS
NONSTRUCTURAL PROTEIN NS
NONSTRUCTURAL PROTEIN NS
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Pred. No. 5.
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יו (WIT-1).
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D (IN REF. 3).
OF61CE6DCCDC5965
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NS1
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\ (OR 1191).
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MEDLINE=91048012; PubMed=2173145;

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A Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buerd K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Stapleton M., Gudin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Pahey J., Helton E., Ketteman M., Madan A., Bockson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Butterfleld Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences.",

Proc. Matl Asad Sci II S. a 301680015001
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PIR; I39287; I39287.
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

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Hypothetical protein; C
SEQUENCE 99 AA; 1153
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STRAIN=CDC 1551 / Oshkosh;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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SUMMARIES

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ALIGNMENTS

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Pfam; PF00207; A2M; 1.

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SEQUENCE 154 AA; 17440 Mn.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
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MEDLINE=9327607; PubMed=8672129;

Winteroe A.K., Fredholm M., Davies W.;

"Evaluation and characterization of a porcine small intestine cDNA"
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Best Local S
Matches 10
                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                046544;
046544;
01-JUN-1998
01-JUN-1998
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9NOM4 PRELIMINARY; PRT; 167 AA.
Q9NOM4;
Q9NOM4;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Complement C3 alpha chain (Fragment).
Cervus nippon (Sika deer).
Cervus nippon (Sika deer).
Charayota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Cervoide;
Cervidae; Cervinae; Cervus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jiang Y., Sun L.G., Yu Y.L.;
Submitted (MAY-2000) to the EMBL/Ge
EMBL; AF264631; AAF73464.1; -.
HSSP; P01024; 1C3D.
InterPro; IPR001599; MacrogloblnA2.
                                                                                                                                                              NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9863;
                                                                                                                                                                                                                                                                                   HSSP;
                                                                                                                                                                                                                                                                                                          J. Immunol. 161:458-466(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                Pfam; PF00207; A2M;
                                                                                                                                                                                                                                                                                                      EMBL; AF038130; AAB92374.2;
                                                                                                                                                                                                                                                                                                                                            "Ubiquitination and dimerization sheep B cells.";
                                                                                                                                                                                                                                                                                                                                                                                     Avila D.
                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=white alpine; TISSUE=Liver; MEDLINE=98309471; PubMed=9647256; Hein W.R., Dudler L., Marston W.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Caprinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Liver;
                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                       Match
    331
                                                                                                                                                                                                                                                            P01024; iC3D.
Pro; IPR001599; MacrogloblnA2
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                                                                                                    Similarity
VKHRILWESASLL 343
                                                                                                                                                                                                                       PS00477; ALPHA_2_MACROGLOBULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKHRILWESASLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITHRIHWESASLL
                                         ITHRIHWESASLL
                                                                                                                                                              349
349 A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 06, Created)
(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
component C3 (Fragment).
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                          349
.; 39679 MW;
                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=9647256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18671
                                                                                                  74.3%;
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                                         13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                               Score 52; DB Pred. No. 0.59

1; Mismatches
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12BFE0798290DFA7
                                                                                                                                                              70C2023E42ED5EE3
                                                                                                                                                                                                                                                                                                                                                                   of complement receptor type
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                                                                                                                    Length 349;
                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        Young
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Best Local
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PRODOM; PD003264; ANAPHYLATOXIN; 1.

SMART; SM00104; ANATO; 1.

SMART; SM00643; C345C; 1.

SMART; SM00643; C345C; 1.

PROSITE; PS00177; ALPHA, 2 MACROGLOBULIN; 1.

PROSITE; PS01177; ANAPHYLATOXIN 1; 1.

PROSITE; PS01177; ANAPHYLATOXIN 2; 1.

SEQUENCE 1661 AA; 186806 MW; 4899D0914E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9HTZ5
Q9HTZ5;
01-MAR-2001
01-MAR-2001
01-JUN-2002
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PRINTS;
ProDom;
SEQUENCE FROM N.A.

STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed-10984043;

MEDLINE-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9GKP1;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9GKP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical PA5194.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
Pseudomonadaceae; Pseudomo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Polymorphic sites in exon 15 and Anim. Genet. 32:46-47(2001). EMBL; AF154933; AAG40565.1; -.
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                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
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InterPro; IPR001840;
InterPro; IPR001599;
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; PF01835; A2M_N;
; PF01821; ANATO;
; PF01759; NTR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITHRIHWESASLL 13
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1 (TrEMBLrel. 16, 1
2 (TrEMBLrel. 21, 1
al protein PA5194.
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ilarity 76.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                               Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anaphylatoxin.
Anaphylatoxn.
MacrogloblnA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Netrin_C.
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16,
23,
                                                                                                                                                                                                                                                                                                                                                                                            Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 52; DB Pred. No. 3; 1; Mismatches
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Last sequence update)
Last annotation updat
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Best Local
                                                                                         01-OCT-2000
01-OCT-2000
01-MAR-2002
                                                                                                                                                           Q9P9Y5;
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InterPro; IPR006224; PSI_RLU;
Pfam; PF00849; PseudoU_synth 2; 1.
ProDom; PD001819; PSI_RLU; 1.
PROSITE; PS01129; PSI_RLU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrer
Hickey M.J., Brinkman F.S.L., Hufinagle W.O., Kowalik D.J., La
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Y.
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., L.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
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Interpro; IRR000326; pA, PTPase.
Pfam; PF01569; PAP2; 1.-
Hypothatical protein; Complete
SEQUENCE 267 AA; 30527 MW;
                                            Hypothetical XF2735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of Pseudomonas aeruginosa PAO1, opportunistic pathogen.";
Nature 406: 959-964 (2000).
EMBL, AB004747; AAG06634.1; -.
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Bacteria, Proteobacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001
01-MAR-2003
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  Bacteria; Proteobacteria;
                         Xylella fastidiosa
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211 AA;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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protein Xf2735.
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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58.3%;
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Gammaproteobacteria; Xanthomonadales;
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Pred. No.
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Pred. No. 19;
                                                                                                                                                                                 PRT;
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57CD9D2319B6AD7D CRC64;
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n S., Yuan Y.,
K., Lim R.M.,
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RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Kitajima J.P.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Manck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Rascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Rascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Rascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA Quaggio R.B., Roberto P.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr.,
RA da Silva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
"The genome sequence of the plant pathogen Xylella fastidiosa.";
Mature 406:151-159(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
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01-JUN-2003 (TrEMBLrel. 23, I
01-MAR-2003 (TrEMBLrel. 23, I
                                                                       Stapleton M., Brokstein P., Hong I., Agbayani A., Carlson J., Chawez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barves M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H. Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M. Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Faccincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
                                                                                                                                                                            STRAIN-Berkeley;
                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hraapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8SYY7; Q9V4I4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Complete SEQUENCE 401 AA; 45544 MW;
                                     Submitted
                                                                                                                                                                                                 SEQUENCE FROM N.A.
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SEQUENCE FROM N
                                                          Celniker S.
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RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Golale R.F.,
RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Batlew R.M., Basu A., Baxer E.G., Helt G., Nelson C.R., Miklos G.I.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews P. Ffannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Shandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
RA de pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA doson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Goldec C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Havey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Haris N.L., Mattei B., McIntosh T.C., McLeod M.-H., Degwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA McIston D.R., Nelson K.A., Naxon K., Nusskern D.R., McCherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Naxon K., Nusskern D.R., Bealeb J.M.,
RA Melson D.R., Nelson K., Saunders R.D.C., Scheeler F., Shen H.,
RA Syirskas R., Tector C., Turner R., Venter T.B., Bolle F., Shen H.,
RA Syles B.C., Stapleton M., Strong R., Sun E.,
RA Syles B.C., Stapleton M., Strong R., Sun E.,
RA Gibbs R.A., Werssaman D.A., Weinstock G.M., Weissenbach J.,
RA Gibbs R.A., Dang F., Zhong W., Zhang G., Zhao
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                                                                                                                                                                                                                   Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Adams M.D., Celniker
Submitted (MAR-2000)
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                                          3ibbs R.A., Rubin C
EMBL/GenBank/DDBJ
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Best Local
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Best Local
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Q8T3J9; Q9VLX7;
01-JUN-2002 (TREMBLRel. 2
01-JUN-2002 (TREMBLREL 2
01-OCT-2002 (TREMBLREL 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q90YC5;
01-DEC-2001
01-DEC-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=21412237; PubMed=11520665;
MEDLINE=21412237; PubMed=11520665;
Hirate Y., Mieda M., Harada T., Yamasu K., Okamoto H.;
"Identification of ephrin-A3 and novel genes specific to the midbrain-
"Identification of ephrin-A3 and novel genes specific to the midbrain-
"Identification of ephrin-A3 and novel genes specific to the midbrain-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ephrin-AJ.
ErNAJ OR EPHRIN-A3.
Brachydanio rerio (Zebrafish) (Danio rer
Brachydanio rekazoa; Chordata; Craniata;
Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AT11889p
CG7196.
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PROSITE;
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Pfam; PF00079; serpin; 1.

PROSITE; PS00284; SERPIN; 1.

Protease inhibitor; Serine protease inhibitor; Serpin.

PROJECT 407 AA; 44863 MW; 5D2A46A75CB6DD78 CRC64;
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Inse
Neoptera, Endopterygota, Diptera, Brachycera,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHB in embryonic zebrafish by o Mech. Dev. 107:83-96(2001). EMBL; AB051678; BAB55891.1; -. EFIN; ZDB-GENE-011108-1; efna3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q90YC5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001799; Ephrin. Pfam; PF00812; Ephrin; 1. PRINTS; PR01347; EPHRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyprinidae;
NCBI TaxID=
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; PS01299; EPHRIN;
E 219 AA; 25146
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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EPHRIN; 1.
25146 MW;
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THE SERPIN FAMILY.
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Pred. No. 37;
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Pred. No. 29;
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      Hexapoda; Insecta; Pterygota; a; Brachycera; Muscomorpha;
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Drosophilidae; Drosophila

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RA Adams C.J., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Hilt R.A., Sabburner M., Henderson S.N.,
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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fuletz S.M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Herrandez J.R., Houck J.,
RA Hashin D., Houston K.A., Howland T.J., Wei M.-H., Degwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M. P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rahert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Sylrskas R., Tector C., Traner R., Venter E., Wang A.H., Wang X.,
RA Harisas R., Tector C., Traner R., Venter E., Wang A.H., Wang X.,
RA Harisas R., Tector C., Traner R., Venter E., Wang A.H., Wang X.,
RA Glibbs R.A., Myers E.M., Shong W., Zhang G., Zhao Q., Zheng L.,
RA Glibs R.A., Wyers E.M., School M., Venter J.C.,
RT The genome sequence of Drosophila melanogaster.";
RN L3 Scheel R. School R. S., Shong W., Zhong Y., Zhao Q., Zheng L.,
RN L3 Scheel R., School R., School R., Smith H.O.,
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                                                         RT Celliker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

A Carlson J., An H., Baldwin D., Banzon J., Beson K.Y., Busam D.A.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Carlson K., Dorsett V., Doup L.B., Doyle C., Dresnek D., Farfan D.,

A Perriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

A Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

A Stapleton M., Strong R., Svirskas R., Tector C., Rubin G.M.;

"Sequencing of Drosophila melanogaster genome.";

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NCBI_TaxID=7227;
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Yu C., Lewis S.E., Rubin G.M.,
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Genome Res. 11.731-753(2001).
EMBL; AE006304; AAK0461; -.
EMBL; AE006304; AAK0471; -.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003140; ABC_TM_transpt.
InterPro; IPR003439; ABC_transporter.
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SMART; SM00382; AAA;
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Bolotin A., Wincker P., Mauger S., Jaillon O.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic aci
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(C STRAIN=16M / ATCC 23456 / Biotype 1;

XX MEDLINE=20020109; PubMed=11756688;

RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., RA Ivanova N., Anderson I., D'Souza M., Bernal A., Mazur M., Goltsmar RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., RA Haselkorn R., Kyrpides N., Overbeek R.;

RT "The genome sequence of the facultative intracellular pathogen RT Brucella melitensis.";

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EMBL, AP005376; BAC09811.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tlr2259 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003
01-MAR-2003
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                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             608
137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      w
                                                                                    Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HRIHWESASLL 13
IRNRTHWNSANL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOVHWPTVSLI
                                         ITHRIHWESASL
                                                                                                                                                                           l protein; Complete
229 AA; 25507 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. (TrEMBLrel.
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                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytosolic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96927 MW;
                                                                                                      57.1%;
58.3%;
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                                         12
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. 20, Last annotation updat
protein BMEI0303.
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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Pred. No. 1.2e
4; Mismatches
                                                                                    2
                                                                                                           Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                      proteome.
98A1769A370F52CA CRC64;
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                                                                                    Mismatches
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                                                                                                           45;
                                                                                                                                BB
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                                                                                                                           Length 229;
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                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                  Letesson J.-J.,
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                                                                                                                                                                                                                                                                                                                                                                           Reznik G.,
                                                                                                                                                                                                                                                                                                                                                         Goltsman E.,
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RESULT 14
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A Kawai J., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Kadachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Butt C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Sabaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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Q9D912;
01-JUN-2001
01-JUN-2001
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conserved hypothetical protein. BR1737.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8FYX0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Pancreas;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brucella suis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Complete SEQUENCE 229 AA; 25507 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22247741; PubMed=12271122;
Paulsen I.T., Seshadri R., Nelson K.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A.
330 / Biovar 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.1%;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB
Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteome.
98A1769A370F52CA CRC64;
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            Wilming L.,
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                                 K. -F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Best Local Similarity
Matches 6; Conser
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EMBL, AK007461; BAB25050.1; -.

MGD; MGI:1923740; 1810012L18Rik.

InterPro; IPR001052; Rubredoxin.

InterPro; IPR007087; Znf C2H2.

SMART; SM00355; ZnF C2H2; 1.

PROSITE; PS00202; RÜBREDOXIN; 1.

SEQUENCE 274 AA; 30610 MW; 4BC
Q8PF47;
Q8PF47;
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q18611;
Q18611;
01-NOV-1996
01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                         "Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ
EMBL; U41030; AAA82366.2; -.
WormPep; C44C1.1; CE27851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bradshaw H., Stellyes L.; "The sequence of C. elegans Submitted (DEC-1995) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Eukaryota; Metazoa; Nematoda; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical C44C1.1.
                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 285 AA; 32140 MW;
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STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              None;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
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Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of
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(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
1 32.1 kDa protein.
(TrEMBLrel. 22,
                                                                                                                                                                                                                                                     Conservative
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                                             PRELIMINARY;
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85.7%;
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75.0%;
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Pred. No. 57;
1; Mismatches
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EMBL/GenBank/DDBJ databases
  Created)
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                                             PRT;
                                                                                                                                                                                                                                                                                                                                             3119FDD3CB1212EE CRC64;
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                                                                                                                                                                                                                                                                                             Length 285;
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Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F., RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A., RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Clapina L.P., RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T., RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A., Formighieri B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira W.C., Oliveira V.R., RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., RA Findade dos Santos M., Truffi D., Tsai S.M., White F.F., Tezza R.I.D., RA Setubal J.C., Kitajima J.P.,
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Q9VRZ4
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Best Local :
STRAINE PECKETEY:
STRAINE PECKETEY:
STRAINE PECKETEY:
MEDLINE 20196006; PubMed = 10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Belson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brottier P.,
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EMBL; AE012064; AAM38974.1; -..
InterPro; IPR001005; Myb DNA binding.
PROSITE; B800334; MYB 2; 1.
Hypothetical protein; Complete protections and analysis of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection o
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidaa; Drosophilidae; Drosophila.
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01-MAR-2003
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STRAIN=306 / ATCC 13902 / XV 101;
STRAIN=306 / ATCC 13902 / XV 101;
MEDLINE=22022145; PubMed=12024217;
da Silva A.C.R., Ferro J.A., Reinach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
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(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation updat
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(TrEMBLrel. 23, Last annotation update)
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Pred. No. 68;
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7B9A97D9C01C60BD CRC64;
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Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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SEQUENCE
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MEDLINE=21192684; PubMed=11296296;

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Q9A017;
SEQUENCE FROM N.A.
STRAIN=MGAS8232 / Serotype M18;
MEDLINE=21927593; PubMed=11917108;
MEDLINE=21927593; PubMed=11917108;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chau Smylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Sarkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang
                                                                                                                                                                                                        Streptococcus pyogenes
Bacteria, Firmicutes;
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TIGRPAMS; TIGR01641; phageSPP1_gp7; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 541 AA; 62314 MW; 5F3DF575EF705BC6
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A Gustincich S., Hill D., Mashiman M., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Wilming L.,
Wynshaw-Boria A. Yoshida K. Haecrawa Y. Kawaii H. Kohteriki S.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local (
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Q9DBV3;
01-JUN-2001
01-JUN-2001
01-MAR-2003
                                                                                     PROSITE; PS00202; RÜBREDOXIN; 1.
ATP-binding; Helicase; Hydrolase.
SEQUENCE 1145 AA; 128624 MW;
                                                                                                                                                                           Pfam; PF00271; helicase C; 1
SMART; SM00487; DEXDC; I.
SMART; SM00490; HELICC; 1.
SMART; SM00355; ZnF_C2H2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR006528; PhageSPP1_gp7.
TIGRRAMS; TIGRO1641; phageSPP1_gp7; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 541 AA; 62419 MW; F6A0DD87C6939473 CRC64;
                                                                                                                                                                                                                                                              MGD; MGI:1918973; 1200013BÓ7Rik.
InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase C.
InterPro; IPR001052; Rubredoxin.
InterPro; IPR007087; Znf C2H2.
Pfam; PF00271; helicase C; 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. EMBL; AE010050; AAL97881.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kapur V., Daly J.A., Veasy L.G., Musser J.M.; "Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Lung; MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 409:685-690(2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wynshaw-Boris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A., Yoshida
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50.0%;
   57.1%;
85.7%;
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17,
23,
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Last sequence update)
Last annotation update)
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   Score 40;
Pred. No.
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Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hasegawa
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                                                                                           A7E1CDED77FED4C0 CRC64;
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   ; DB 11;
. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse
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                           Length 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collection.";
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RESULT NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE NEESTLE
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SEQUENCE FROM N.A.

SEQUE
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Best Local
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                                                                                                                                                                                                                                                                                                                                      Q9HK18;
Q9HK18;
01-MAR-2001
01-MAR-2001
01-MAR-2003
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01-OCT-2002
01-OCT-2002
01-OCT-2002
                                                                                                                                                              TA0790.
Thermoplasma acidophilum.
Archaea; Euryarchaeota; Thermoplasmata;
Archaea; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Setubal J.C., Kitajıma v..., "Comparison of the genomes of two
STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
Ruepp A., Graml W., Santos-Martinez M.-L.,
                                                                                                                                                                                                                                                                                                             Endonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical
SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 417:459-463(2002).
EMBL; AE011637; AAM35030.1;
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                  NCBI_TaxID=2303;
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5; Conserv
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172 AA; 18689 MW;
                                                                                                                                                                                                                                                                                             (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
s III related protein.
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45.5%;
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Last annotation updat
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5A62A85829AD9718 CRC64;
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50;
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RESULT 25
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat.
Hypothetical protein R03328.
R03328 OR SMC04094
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Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Boistard P., Becker A., Bourry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Penard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Sinorhizoblum meilloti strain 1021."; Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
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Pfam; PF00730; HhH-GPD; 1.
SMART; SM00478; ENDO3c; 1.
SMART; SM00525; FES; 1.
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Nature 407:508-513(2000)
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HSSP; P20625; 2ABK.
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Bacteria; Proteobacteria; Alphaproteobacteria;
Rhizobiaceae; Sinorhizobium.
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InterPro; IPR003265; Endo 3c.
InterPro; IPR003551; FeS bind.
InterPro; IPR000445; HhH.
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197 AA; 22753 MW;
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Created)
Last sequence update)
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Pred. No. 58;
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C73E5DB05764FD67 CRC64;
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Pfam; PF00001; 7tm_1; 1.
PROSITE; PS00237; G_PROTSIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTSIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21435808; PubMed=11551509; Dong X., Han S.-K., Zylka M.J., Simon M.I., The Diverse Family of GPCRs Expressed in Spec Nociceptive Somatosensory Neurons."; Cell 106:619-632(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G protein-coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6;
MEDLINE=21435808; PubMed=11551509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRGB5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                               Pfam; PF00001; 7tm_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AY042202; AAK91798.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                             EMBL; AY042203; AAK91799.1; -
                                                                                                                                                                                                                                                                                                                               Nociceptive Somatosensory Neurons."; Cell 106:619-632(2001).
                                                                                                                                                                                                                                                                                                                                                                        Dong X., Han S.-K., Zylka M.J., Simor
"A Diverse Family of GPCRs Expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                             InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein-coupled receptor.
  284
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                                                                                    Similarity 6; Conserv
HRLQWQSLKLL
                                         HRIHWESASLL 13
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                                                                                                                                                                             322 AA;
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                                                                                      Conservative
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294
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Last annotation updat
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Pred. No.
                                                                                                             Score 39;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CBDF185B470DB8B4 CRC64;
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                                                                                         Mismatches
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                                                                                                                               Length 322;
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RESULT 27 Q8RTQ7 ID Q8RTQ

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       Q8CJT5;
Q8CJT5;
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Q93EV7;
Q1-DEC-2001
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Bacteria; Thermodesulfobacteriales;
Thermodesulfobacteriaceae; Thermodesulfobacterium.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Dissimilatory sulfite reductase alpha subunit (Fragment).
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Submitted (MAY-2000) to the EMBL/G
EMBL; AF271771; AAL78311.1; -.
InterPro; IPR066067; Nir_Sir_4Fe4S
Pf4m; PF01077; NIR_SIR; I.
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01:98:imilatory sulfite reductase alpha subunit (Fragment).
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Bacteria; Thermodesulfobacteria; Thermodesulfobacteriales;
Thermodesulfobacteriaceae; Thermodesulfobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between Major Lineages of Sulfate-Reducing J. Bacteriol. 183:6028-6035(2001).
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Abicht H., Blackall L.L., Stahl D.A., Wagner M.;
"Multiple Lateral Transfers of Dissimilatory Sulfite Reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=DSM 2178,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Pfam; PF01077; NIR SIR; I.
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       (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                              95
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Created)
Last sequence update)
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Pred. No. 1.1e+02;
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Pred. No. 1.1e+02;
4; Mismatches (
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                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                           Ouchane S., Picaud M., Vernotte C., Reiss-Husson F. "Pleiotropic effects of puf interposon mutagenesis biosynthesis in Rubrivivax gelatinosus. A new gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL939120; CAD55486.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 387 AA; 44420 MW; D842730E90A97C4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harris D.E., Quail M.A., Kieser H., Collins M., Erown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                  STRAIN=S1;
                                                                                                                                                                                                                                                                                                                                      Comamonadaceae;
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                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=28068;
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MEDLINE=21996410; PubMed=12000953;
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U73944; AAC44799.1; -.
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Nagashima K.V., Matsuura K., Ohyama S., Shimada K.;
"Primary structure and transcription of genes encoding B870
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    SEQUENCE
                                                                                       NCBI_TaxID=152794;
                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacterium.
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Biochemistry 38:15238-15244(1999).
EMBL; AB034704; BAA94047.1; -.
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Q8E3H4;
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[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=NEM316 / Serotype III;
STRAINE=22242508; PubMed=12354221;
MEDLINE=22242508; PubMed=12354221;
MEDLINE=22242508; PubMed=12354221;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Methionyl-tRNA synthetase beta subunit. 6/101.
Dictyostellum discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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EMBL; AP005214; BAC16943.1; -.
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Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi
Usuda Y., Sugimoto S.;
                                                                                                                                                                                                                                                                                                                                                  Hypothetical GBS1785.
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                                                                                                                                                                                                                                                                      Bacteria; Firmicutes;
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TIGRFAMS; TIGRO0449; tgt general; 1.
SEQUENCE 437 AA; 49833 MW; 7AFF7555D99427A6 CRC64;
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InterPro; IPR002616; tRNA_ribo_trans.
Pfam; PF01702; TGT; 1.
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Q8DXV6;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=2603 V/R / Serotype V;
MEDLINE=22222988; PubMed=12200547;
Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S. Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Carty H.A., Cline R.T., Van Aken S.B., Gill J., Scarselli M., Mora Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G., "Crasslic."
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
CydC protein.
CYDC OR LIN2864.
Listeria innocua.
Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
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Mol. Microbiol. 45:1499-1513(2002).
EMBL, ALTG6853; CAD47444.1; -..
SagaList; gbs1785; -.
SagaList; gbs1785; -.
Hypothetical protein; Complete proteome.
SEQUENCE 572 AA; 64458 MW; 9CB68B07FA063F9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence and comparative genomic analysis of a emerging human pathogen, serotype V Streptococcus agalactiae.", Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP-binding; Complete proteome. SEQUENCE 572 AA; 64423 MW;
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STRAIN=2603 V/R /
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fishi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Mordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann B., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
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Gautier L., Goebel W., Gomez-Dez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Mordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
                                                                                                               Science 294:849-852(2001).
EMBL; AL591984; CAD00929.1; -.
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MEDLINE=21537279; PubMed=11679669;
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Bacteria; Firmicutes; E
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PubMed=11679669;
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        IPR003593;
IPR001140;
IPR003439;
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; ABC_TM_transpt.
; ABC_transporter.
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AAA ATPase.
ABC_TM_transpt.
ABC_transporter.
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Last annotation update)
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Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B5B3A9758CAF8B98 CRC64;
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RESULT 39
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Best Local
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Best Local :
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SMART; SM00382; AAA;
Complete proteome.
SEQUENCE 574 AA; 6:
TISUE=Spinal cord;
Rerbajinal W., Arahata K., Tsukahara T.;
"Increased expression level of a novel alternative splic
SIP1 in motor neuron diseases.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AB037701; BAB03508.1; -.
InterPro; IPR007022; SIP1.
Pfam; PP04938; SIP1; 1.
                                                                                                                                                                                                                   Q9NS79
Q9NS79;
01-OCT-2000
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                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Spinal cord;
Aerbajinai W., Arahata K., Tsukahara T.;
Merbajinai W., Arahata K., Tsukahara T.;
"Increased expression level of a novel alternative splicing variant of SIP1 in motor neuron diseases.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
SMN interacting protein 1-gamma.
                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                  SMN interacting
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Pfam; PF04938; SIP1; 1.
SEQUENCE 250 AA; 28155
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
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Mammalia; Eutheria;
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                                                                                                                                                              Homo
                                                                                                                         NCBI_TaxID=9606;
                                                                                                     EQUENCE FROM N.A.
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                                                                                                                                                            sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TaxID=9606;
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Primates;
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83.3%;
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L; Mismatches 0
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                                                                  alternative splicing
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1.1e+02
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Best Local S
Matches 6
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Best Local S
Matches 7
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
17-JUN-2002 (TrEMBLrel. 21, Last sequence update)
17-JUN-2002 (TrEMBLrel. 21, Created)
17-JUN-2002 (TrEMBLrel. 21, Last sequence update)
17-JUN-2002 (TrEMBLrel. 21, Created)
17-JUN-2002 (TrEMBLrel. 21, Last sequence update)
17-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.;
"Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefactens C58.";
Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8UBV4;
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                                                                                                                                                                                                                                                                                                                   EMBL; AE009222; AAL43727.1; ALT_INIT.
EMBL; AE008188; AAK88461.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 266 AA; 29620 MW; 40B98CC626C43B27 CRC64;
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MEDLINE=21608551; PubMed=11743194;
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Alphaproteobacteria; Rhizobiales;
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Pred. No.
                                                                                                                                                         Score 38; DB 16;
Pred. No. 1.2e+02;
L; Mismatches 4
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